

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 11:54:20 ; Search time 40 Seconds  
(without alignments)  
536.408 Million cell updates/sec

Title: US-10-665-602-2  
Perfect score: 1249  
Sequence: 1 MTWRHHVRLFTVSLAQII.....PSVLQRRRPGRPLGHRL 223

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267	21.4	171	2 I49612	teratocarcinoma-de
2	233	18.7	188	2 A30362	teratocarcinoma-de
3	225	18.0	188	2 A39787	teratocarcinoma-de
4	123	9.8	4391	2 A38096	perlecan precursor
5	121.5	9.7	1620	2 T37283	hypothetical prote
6	120.5	9.6	722	2 I48324	DLTA-like 1 - mou
7	120.5	9.6	1372	2 T25933	hypothetical prote
8	119	9.5	810	2 T10756	Nel-homolog protei
9	118	9.4	2703	1 A24420	notch protein - h
10	116.5	9.3	2321	2 S78549	notch3 protein - h
11	115.5	9.2	2555	2 A40043	notch protein homo
12	114.5	9.2	1574	2 T13954	MSGF6 protein - ra
13	114	9.1	1687	2 T30176	Egr repeat transme
14	113.5	9.1	1964	2 T09059	notch4 - mouse
15	113.5	9.1	2437	2 S42612	transmembrane prot
16	112.5	9.0	1251	2 A57293	latent transformin
17	112.5	9.0	2524	2 A35844	Xotch protein - Af
18	111	8.9	728	2 T50719	C-Delta-1 - chicke
19	111	8.9	833	2 S19087	Gene Delta protein
20	111	8.9	861	2 A48825	Notch homolog Motc
21	111	8.9	1722	2 E98753	protein Fl1C7.4 [i
22	111	8.9	2531	2 S18188	notch protein homo
23	111	8.9	2531	2 A46019	notch-1 protein -
24	111	8.9	3707	2 S18232	heparan sulfate pr
25	110	8.8	2318	2 S45306	notch 3 protein -
26	109	8.7	2471	2 A49128	cell-fate determin
27	108	8.6	832	2 A31246	neurogenic protein
28	108	8.6	880	2 S00670	neurogenic repetit
29	106	8.5	1810	1 A32230	tenascin precursor

30	105	8.4	615	1 KF0U12	coagulation factor
31	104.5	8.4	387	2 B49175	Motch A protein -
32	104	8.3	513	2 D88991	protein apx-1 [imp
33	103.5	8.3	835	2 JP0076	nel protein - chic
34	103	8.2	379	2 A59180	Wnt inhibitory fac
35	102.5	8.2	1064	2 A40136	fibropellin Ia - s
36	102.5	8.2	3002	2 A47221	fibroblast 1 precu
37	102.5	8.2	3871	2 T22812	fibroblast 1 precu
38	102	8.2	907	2 T15792	hypothetical prote
39	102	8.2	1295	2 A32901	gip1 protein presu
40	101.5	8.1	477	2 J50597	t-plasminogen acti
41	101.5	8.1	1203	2 A49175	Motch B protein -
42	101.5	8.1	2871	2 A55567	fibroblast 1 - bovi
43	101.5	8.1	2871	2 A55624	fibroblast 1 - bovi
44	101.5	8.1	5376	2 T42215	zonadhesin - mouse
45	101	8.1	401	2 S65138	glycoprotein anti

ALIGNMENTS

RESULT 1

I49612  
teratocarcinoma-derived growth factor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49612  
R:Donor, R.; Scalera, L.; Pacifico, F.; Simeone, A.; Persico, M.G.; Acampora, D.  
Development 118, 1157-1168, 1993  
A:Title: The murine cripto gene: expression during mesoderm induction and early heart m  
A:Reference number: I49612; MUID:94094736; PMID:7916676  
A:Accession: I49612  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-171 <RES>  
A:Cross-references: UNIPROT:PS1865; UNIPARC:UPI00000029326; GB:M87321; NID:9402714; PIDN:  
C:Genetics:  
A:Gene: cripto  
C:Superfamily: teratocarcinoma-derived growth factor 1; EGF homology

Query Match	21.4%	Score 267;	DB 2;	Length 171;
Best Local Similarity	37.8%	Pred. No. 9.7e-16;		
Matches	56;	Conservative	11;	Mismatches 63; Indels 18; Gaps 3;
Qy	58	FGVETG-----SAEGWGPEEPYPYSAF-----	-----GEGASARPRCRNGGTCVLGSFC	103
Db	20	FGPVAGRDLAIRDNSIWDQKEPAVRDRSFQVPSVQNSKSLNKTCLNGGTCILGSFC	79	
Qy	104	VCPAHFTGRYCEHDORSECGALEHGAWTURACHLCRCIFGALHCLPLQTPDRCD----	P 159	
Db	80	ACPPSFYGRNCEHDVRKEHCGSLHGTWLPKKSCLRCWGHQHLCLPOTFLPGCDGHVMD	139	
Qy	160	KDFLASHAHGFSAGGAPSLLLLLPCALL	187	
Db	140	QDLKASRTPCQTPSVTTTFMLAGACFL	167	

RESULT 2

A30362  
teratocarcinoma-derived growth factor 1 - human  
N:Alternate names: CRIPTO protein  
C:Species: Homo sapiens (man)  
C:Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 09-Jul-2004  
C:Accession: B39787; A30362  
R:Donor, R.; Montuori, N.; Rocchi, M.; De Ponti-Zilli, L.; Ciccodicola, A.; Persico, M.G.  
Am. J. Hum. Genet. 49, 555-565, 1991  
A:Title: Isolation and characterization of the CRIPTO autosomal gene and its X-linked re  
A:Reference number: A39787; MUID:91353571; PMID:1882841  
A:Accession: B39787  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-188 <DON>  
A:Cross-references: UNIPROT:P13385; UNIPARC:UPI000004966D; GB:M96955; GB:M37099; NID:933



F;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carboxylate (Asn) (coval)  
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 9.8%; Score 123; DB 2; Length 4391;  
Best Local Similarity 27.3%; Pred. No. 0.037;  
Matches 39; Conservative 4; Mismatches 42; Indels 58; Gaps 4;

QY 85 SARPCRCRNGGTC---VLGSFVCVCPAHFTGRYCEHQRSECCGALEHGAWTLRACHLCR 140  
DB 3847 TCDRPFQNGQGCHDSESSYVVCVCPAGFTGSRCEHSQ-----3884

QY 141 CIFGALHCLPLQTPDRCDPKDFLASHAG-----PSAGGAP 176  
DB 3885 ----ALHC-----HPEACGPDATCVNRPDGRGYTCRCHLGRSLRCBEGVTVTTPSLSGAG 3936

QY 177 SLILLPCALLHLLRLRPDAPHP 199  
DB 3937 SYLALPALTNTHRLDLDFEKP 3959

RESULT 5  
T27283  
hypothetical protein Y64G10A.f - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T27283  
R;Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20336  
A;Accession: T27283  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1620 <NIL>  
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1;  
A;Experimental source: clone Y64G10A  
C;Genetics:  
A;Gene: CESP:Y64G10A.f  
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 9.7%; Score 121.5; DB 2; Length 1620;  
Best Local Similarity 26.6%; Pred. No. 0.02;  
Matches 47; Conservative 14; Mismatches 63; Indels 53; Gaps 8;

QY 51 LNMVTSHFGEVTSAAE-----GWPPEELPVSRAFGEGAS-----ARPCRCRN 93  
DB 28 LNFTSIFRREL-GEIEKLDLFPNFHARKYLRFARFSRRGCGKCCLLRVQANCSADLCHN 86

QY 94 GGTCVLG-----SFCVCPAHFTGRYCEHQRSECCGALEHGAWTLRACHLCRCIF 143  
DB 87 GGTCTPSEHNDNEQVCECPVGTGAKCYD--ANECMANNNGGCEHCWNTIGTYTCRCWP 144

QY 144 G-----ALHCLPLQTPDRCDPKDFLASHAGPSAGGAPS 177  
DB 145 GFELSGDNGTCSDDIECAVNSGGCDRCVNSPGFRCDCPSDLVLHADGRTCGKVT 201

RESULT 6  
I48324  
DELTA-like 1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48324  
R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.  
Development 121, 2407-2418, 1995  
A;Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin  
A;Reference number: I48324; MUID:95401850; PMID:7671806  
A;Accession: I48324  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-722 <RES>  
A;Cross-references: UNIPROT:Q61483; UNIPARC:UPI0000028700; EMBL:X80903; NID:G806569; PID

A;Gene: Dll1  
C;Superfamily: delta-4 protein; EGF homology  
F;331-362/Domain: EGF homology <EGF2>  
F;446-477/Domain: EGF homology <EGF>  
F;484-515/Domain: EGF homology <EGF1>

Query Match 9.6%; Score 120.5; DB 2; Length 722;  
Best Local Similarity 30.0%; Pred. No. 0.012;  
Matches 45; Conservative 8; Mismatches 56; Indels 41; Gaps 8;

QY 91 CRNGGTC---VLGSFVCVCPAHFTGRYCEHQRSECCGALEHGAWTLRACH----LCRC 141  
DB 451 CANGGTCRDSVNDFTCTPPGYTKNCSAPVSRCEHAPCHNGA-----TCHQRQRYNCEC 506

QY 142 I--FGALHC---LPLQTPDRCDPKDFLASHAGPSAGG-----APSLLLLLPCA 185  
DB 507 AQYGGPNCOFLPEPPP---GMVVDLSERHNSQGGPPVAVCAGVVLVLLLLGCA 563

QY 186 LLHRLRPDAPAHPRSLVPSVLRERRPCG 215  
DB 564 AVVVCVRLKLQKH-----QPPPEPCG 584

RESULT 7  
T25933  
hypothetical protein W02C12.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T25933  
R;Murray, J.; Wohldmann, P.  
submitted to the EMBL Data Library, December 1996  
A;Description: The sequence of C. elegans cosmid W02C12.  
A;Reference number: Z20112  
A;Accession: T25933  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1372 <MUR>  
A;Cross-references: UNIPROT:P91526; UNIPARC:UPI0000075513; EMBL:U80815; PIDN:AAB37995.1;  
A;Experimental source: strain Bristol N2; clone W02C12  
C;Genetics:  
A;Gene: CESP:W02C12.1  
A;Map position: 4  
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 9.6%; Score 120.5; DB 2; Length 1372;  
Best Local Similarity 37.1%; Pred. No. 0.021;  
Matches 36; Conservative 7; Mismatches 35; Indels 19; Gaps 6;

QY 85 SARPCRC---CRNGGTCVLGSF-----CVCVPAHFTGRYCEHQRSECCGALEHGAWTLRA 135  
DB 293 SAPNRICIGQPCHNGGEC--GDFGSHLEACAPASFTGKGEF--KNTGCKTCENGKCAEA 348

QY 136 C-HLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPS 171  
DB 349 AGGLQRC-----ECSPGFTGCERTNIDECSTAHCP 380

RESULT 8  
T10756  
Nel-homolog protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T10756  
R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsuhashi, S.; Kikkawa, U.  
submitted to the EMBL Data Library, November 1998  
A;Description: Protein kinase C-binding protein.  
A;Reference number: Z17122  
A;Accession: T10756  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-810 <KUR>  
A;Cross-references: UNIPROT:Q62919; UNIPARC:UPI000012FF2B; EMBL:U48246; NID:G3851179; PID

Query Match 9.58; Score 119; DB 2; Length 810;  
Best Local Similarity 39.24; Pred. No. 0.018;  
Matches 29; Conservative 6; Mismatches 25; Indels 14; Gaps 4;  
QY 81 GEGASARPRC---CRNGGTCVLGSCFVCVCPAHTGTRYCEHDQRRSECCGALFHGAWTLRACH 137  
Db 510 GNGTICKAFCEGCRYGGTCVAPKVCPSGFGTGSCKEIDIDCABGFVE-----CH 561  
QY 138 -LCRCIF--GALHC 148  
Db 562 NYSRCVNLPGWYHC 575  
RESULT 9  
A24420  
notch protein - fruit fly (Drosophila melanogaster)  
N;Alternate names: neurogenic repetitive locus protein  
C;Species: Drosophila melanogaster  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Oct-2004  
C;Accession: A24420; A24768; S093358; A05267  
R;Kidd, S.; Kelley, M.R.; Young, M.W.  
Mol. Cell. Biol. 6, 3094-3108, 1986  
A;Reference number: A24420; MUID:87064624; PMID:3097517  
A;Accession: A24420  
A;Molecule type: DNA  
A;Residues: 1-2703 <KID>  
A;Cross-references: UNIPROT:P07207; UNIPARC:UPI000016BC6; GB:K03508; NID:gi157991; PIDN:  
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.  
Cell 43, 567-581, 1985  
A;Reference number: A24768; MUID:86079539; PMID:3935325  
A;Accession: A24768  
A;Molecule type: mRNA  
A;Residues: 1-48, '1', '50-118', 'R', '120-230', 'I', '232-256', 'N', '258-266', 'A', '268-872', 'R', '874-958',  
A;Cross-references: UNIPARC:UPI0000173D1F  
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044  
R;Tautz, D.  
Nucleic Acids Res. 17, 6463-6471, 1989  
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma  
A;Reference number: S09358; MUID:89385974; PMID:2780284  
A;Accession: S09358  
A;Molecule type: DNA  
A;Residues: 2505-2551, 'QQQQ', '2552-2576', 'E', '2578-2604 <TAU>  
A;Cross-references: UNIPARC:UPI0000173D20  
R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.  
Cell 40, 55-62, 1985  
A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other  
A;Reference number: A05267; MUID:85099329; PMID:2981631  
A;Accession: A05267  
A;Molecule type: DNA  
A;Residues: 2504-2576, 'E', '2578-2611 <WHA2>  
A;Cross-references: UNIPARC:UPI0000173D21  
C;Genetics:  
A;Gene: notch; opa  
A;Cross-references: FlyBase:FBgn0004647  
A;Map position: 8.96-9.36  
A;Intons: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
C;Keywords: differentiation; tandem repeat; transmembrane protein  
F;27-43/Domain: transmembrane #status predicted <TM1>  
F;297-328/Domain: EGF homology <EGF1>  
F;530-561/Domain: EGF homology <EGF1>  
F;568-599/Domain: EGF homology <EGF>  
F;988-1019/Domain: EGF homology <EGX2>  
F;1064-1095/Domain: EGF homology <EGF3>  
F;1187-1218/Domain: EGF homology <EGX3>  
F;1746-1762/Domain: transmembrane #status predicted <TM2>  
F;1950-1982/Domain: ankyrin repeat homology <AN1>  
F;1983-2015/Domain: ankyrin repeat homology <AN2>  
F;1988-2004/Domain: transmembrane #status predicted <TM3>  
F;2017-2049/Domain: ankyrin repeat homology <AN3>  
F;2050-2082/Domain: ankyrin repeat homology <AN4>  
F;2083-2115/Domain: ankyrin repeat homology <AN5>

F;2538-2568/Region: glutamine-rich  
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>  
Query Match 9.4%; Score 118; DB 1; Length 2703;  
Best Local Similarity 34.6%; Pred. No. 0.064;  
Matches 28; Conservative 13; Mismatches 24; Indels 16; Gaps 6;  
QY 91 CRNGGTCVL---GSFCVCPAHTGTRYCEHDQRRSECCGAL--EHGAW---TLRACH---L 138  
Db 67 CQNGGTCVTLNGKTYCADCSDHYVDYCEH---RNPFCNSMRCONGGTCQVTFRNHGPGIS 123  
QY 139 CRCIFGALHCL-PLQTPDRCD 158  
Db 124 CKCPLGFDSELCIEIAPNACD 144  
RESULT 10  
S78549  
notch3 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: S78549; S71825  
R;Joutel, A.; Tournier-Lasserre, E.  
submitted to the EMBL Data Library, April 1997  
A;Reference number: S78549  
A;Accession: S78549  
A;Molecule type: mRNA  
A;Residues: 1-2321 <JOUI>  
A;Cross-references: UNIPROT:Q9UMA7; UNIPARC:UPI000011D827; EMBL:U97669; NTD:G2668591; PFI  
R;Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowitc  
x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.  
Nature 383, 707-710, 1996  
A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke  
A;Reference number: S71825; MUID:97032728; PMID:8878478  
A;Accession: S71825  
A;Molecule type: DNA  
A;Status: nucleic acid sequence not shown  
A;Residues: 67-113;138-194;268-333, 'G', '335-346;536-613;716-765;1240-1279;1815-1888 <JOUI2>  
A;Cross-references: UNIPARC:UPI0000177457; UNIPARC:UPI0000177458; UNIPARC:UPI0000177459;  
C;Genetics:  
A;Gene: notch3  
A;Map position: 19p13.1  
C;Function:  
A;Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
C;Keywords: tandem repeat; transmembrane protein  
F;123-155/Domain: EGF homology <EGX1>  
F;162-194/Domain: EGF homology <EGF1>  
F;240-271/Domain: EGF homology <EGX2>  
F;318-349/Domain: EGF homology <EGF>  
F;473-504/Domain: EGF homology <EGX3>  
F;853-884/Domain: EGF homology <EGF3>  
F;928-959/Domain: EGF homology <EGX4>  
F;1838-1870/Domain: ankyrin repeat homology <AN1>  
F;1871-1903/Domain: ankyrin repeat homology <AN2>  
F;1908-1937/Domain: ankyrin repeat homology <AN3>  
F;1938-1970/Domain: ankyrin repeat homology <AN4>  
F;1971-2003/Domain: ankyrin repeat homology <AN5>  
Query Match 9.3%; Score 116.5; DB 2; Length 2321;  
Best Local Similarity 32.3%; Pred. No. 0.075;  
Matches 43; Conservative 5; Mismatches 50; Indels 35; Gaps 9;  
QY 69 GPEELPYSRAFEGEGASAPRCRCRNGTCV--LGSP-CVCPAHTGTRYCEHDQRRSECGA 125  
Db 1165 GFGPPL-----DSGPRCLHN-GTCVDLVGGPRCTCPGTYTLRCEADINECRSGA 1213  
QY 126 LSHGAWTLRAC-----HLRCIFGALHCLPLQTPDRCDPKDFLASHAHG-----PSA 172  
Db 1214 C-HAART-RDCLQDPGGGPRCLCHAGFSGPRCQTVLSPCESQPCQ-----HGGQCRPSP 1265  
QY 173 GGAPSLLLLLPCA 185

[illegible]

QY 130 AWTLRACH-----LCRCIFGALH--CLPLQTPDRCD----- 158  
Db 1009 -----RCHPSGTAAACHSLANAFYQCCLPGHTGQRCVEWMDLCOQPCSNNGSCEITGPP 1064  
QY 159 -----PKDF-----LASHAHGPSAGGAPSLLLLP-----CALLHRLLRP 193  
Db 1065 PGFTCHCPKGFEGPTCSHKALSCGIIHHCHNGG-----LCLPSPKPGSPPLCACLSGFGGP 1119  
QY 194 DA---PAHPRSLVPSVLQRRRPC-----GRPGLGH 221  
Db 1120 DCLTPPAPGCGPPS-----PCLHNGTCTETPGLGN 1150  
RESULT 15  
S42612  
transmembrane protein precursor - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S42612  
R:Bierkamp, C.; Campos-Ortega, J.A.  
Mech. Dev. 43, 87-100, 1993  
A:Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern  
A:Reference number: S42612; MUID:94128602; PMID:8297791  
A:Accession: S42612  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2437 <BIE>  
A:Cross-references: UNIPROT:P46530; UNIPARC:UPI0000130565; EMBL:X69088; NID:9433866; PID  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F:755-786/Domain: EGF homology <EGF1>  
F:1023-1054/Domain: EGF homology <EGF>  
F:1185-1216/Domain: EGF homology <EGF2>  
F:1915-1947/Domain: ankyrin repeat homology <AN1>  
F:1948-1980/Domain: ankyrin repeat homology <AN2>  
F:1982-2014/Domain: ankyrin repeat homology <AN3>  
F:2015-2047/Domain: ankyrin repeat homology <AN4>  
F:2048-2080/Domain: ankyrin repeat homology <AN5>  
Query Match 9.1%; Score 113.5; DB 2; Length 2437;  
Best Local Similarity 39.5%; Pred. No. 0.14;  
Matches 32; Conservative 7; Mismatches 19; Indels 23; Gaps 7;  
QY 88 PRC-----CRNGGTCV--LGSF-CVCPAHTGYRCEHDQRSEC-----GALEHGAWT 132  
Db 983 PDCTESSCFNGTCVDGIGSFSVCULFGFTGNYCQHDV--NECDSPCQNGSCQDGYGT 1040  
QY 133 LRACHLCRCIFG--ALHCLPL 151  
Db 1041 YK----CTCPHYGTGLNCQSL 1057

Search completed: September 7, 2006, 11:59:50  
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: September 7, 2006, 11:51:00 ; Search time 297 Seconds  
(without alignments)  
694,540 Million cell updates/sec

Title: US-10-665-602-2  
Perfect score: 1249  
Sequence: 1 MTRWHVRLFTVSLALQII.....PSVLQRRRRCGRPGIGHRL 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1241	99.4	223	1 CFC1_HUMAN	O9gzt3 homo sapien
2	488	39.1	202	1 CFC1_MOUSE	P97766 mus musculus
3	322.5	25.8	193	1 CFC1_CHICK	O9i8q3 gallus gall
4	286	22.9	183	2 Q504I5_BRARE	Q504I5 brachydanio
5	285	22.8	183	2 Q57517_BRARE	O57517 brachydanio
6	275.5	22.1	190	2 Q57516_BRARE	O57516 brachydanio
7	269	21.5	179	2 Q2VU94_XENLA	Q2VU94 xenopus lae
8	267	21.4	171	1 TDGF1_MOUSE	P51865 mus musculus
9	265	21.2	171	2 Q3UZP8_MOUSE	Q3UZP8 mus musculus
10	265	21.2	171	2 Q7TQ06_MOUSE	Q7TQ06 mus musculus
11	263	21.1	191	2 Q2U296_XENLA	Q2U296 xenopus lae
12	261.5	20.9	251	2 Q2U294_XENLA	Q2U294 xenopus lae
13	261.5	20.9	251	2 Q2VU93_XENLA	Q2VU93 xenopus lae
14	261	20.9	191	2 Q2VU96_XENLA	Q2VU96 xenopus lae
15	249.5	20.0	190	2 Q2U297_XENLA	Q2U297 xenopus lae
16	248.5	19.9	190	2 Q800J2_XENLA	Q800J2 xenopus lae
17	248.5	19.9	190	2 Q91649_XENLA	Q91649 xenopus lae
18	242	19.4	181	2 Q58D57_BOVIN	O58D57 bos taurus
19	233	18.7	188	1 TDGF1_HUMAN	P13385 homo sapien
20	233	18.7	188	2 Q8TCC1_HUMAN	O8TCC1 homo sapien
21	225	18.0	188	1 TDGF2_HUMAN	P51864 homo sapien
22	178	14.3	66	2 Q91AT2_BRARE	Q91AT2 brachydanio
23	135	10.8	763	2 Q4VB88_HUMAN	Q4VB88 homo sapien
24	135	10.8	763	2 Q4VB91_HUMAN	Q4VB91 homo sapien
25	134.5	10.8	2061	2 Q4SRM9_TETNG	Q4SRM9 tetraodon n
26	132	10.6	164	2 Q4RQ94_TETNG	Q4RQ94 tetraodon n
27	130.5	10.4	714	1 DLLL_RAT	P97677 rattus norv
28	130.5	10.4	772	1 DLLA_BRARE	O6d148 brachydanio
29	130	10.4	737	2 Q6IR63_XENLA	Q6IR63 xenopus lae
30	127.5	10.2	834	2 Q52KG8_MOUSE	O52KG8 mus musculus
31	127	10.2	566	2 Q4SPK6_TETNG	Q4SPK6 tetraodon n

32	127	10.2	780	2	Q6DJD9_XENLA	O6djd9 xenopus lae
33	125.5	10.0	512	2	Q95RQ1_DROME	Q95rq1 drosophila
34	125	10.0	238	2	Q8QGG9_CHICK	O8qgg9 gallus gall
35	125	10.0	738	2	Q90Z45_CHICK	O90z45 gallus gall
36	123	9.8	351	2	Q2VPA1_HUMAN	Q2vpa1 homo sapien
37	123	9.8	810	1	NELL1_HUMAN	Q92832 homo sapien
38	123	9.8	810	2	Q4VB90_HUMAN	Q4vb90 homo sapien
39	123	9.8	810	2	Q6NSY8_HUMAN	O6nsy8 homo sapien
40	123	9.8	2331	2	Q59EG0_HUMAN	O59eg0 homo sapien
41	123	9.8	4391	1	PGBM_HUMAN	P98160 homo sapien
42	123	9.8	4391	2	Q5VU27_HUMAN	O5vu27 homo sapien
43	121.5	9.7	2067	2	Q59ED8_HUMAN	O59ed8 homo sapien
44	121.5	9.7	2555	2	Q5SXM3_HUMAN	O5sxm3 homo sapien
45	121	9.7	1651	2	Q9TVQ2_CABEL	Q9tvq2 caenorhabdi

ALIGNMENTS

RESULT 1  
ID\_CFC1\_HUMAN STANDARD; PRT; 223 AA.  
AC Q9GZR3; Q53T05;  
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.  
DT 01-MAR-2001, sequence version 1.  
DT 07-MAR-2006, entry version 32.  
DE Cryptic protein precursor.  
GN Name=CFC1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], FUNCTION, VARIANT HTX2  
RP CYS-112, CHARACTERIZATION OF VARIANT HTX2 CYS-112, AND VARIANTS TRP-78  
RP AND CYS-189.  
RX MEDLINE=20517351; PubMed=11062482; DOI=10.1038/81695;  
RA Bamford R.N., Roessler E., Burdine R.D., Saplakoglu U., dela Cruz J.,  
RA Splitt M., Towbin J., Bowers P., Marino B., Schier A.F., Shen M.M.,  
RA Muenke M., Casey B.;  
RA "Loss-of-function mutations in the EGF-CFC gene CFC1 are associated  
RT with human left-right laterality defects.";  
RL Nat. Genet. 26:365-369(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANT TRP-78.  
RX PubMed=15815621; DOI=10.1038/nature03466;  
RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H.,  
RA Minx P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,  
RA Becker M.C., Fewell G.A., Delehaanty K.D., Miner T.L., Nash W.E.,  
RA Kremitzki C., Oddi L., Du H., Sun H., Bradshaw-Cordum H., Ali J.,  
RA Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C.,  
RA Du F., Courtney L., Kallicki J., Ozersky P., Abbott S., Armstrong J.,  
RA Belter E.A., Caruso L., Cedroni M., Cotton M., Davidson T., Desai A.,  
RA Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K.,  
RA Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong C.M.,  
RA Grewal N., Goyea E., Hou S., Levy A., Martinka S., Mead K.,  
RA McCellan M.D., Meyer R., Randall-Maher J., Tomlinson C.,  
RA Dauphin-Kohlberg S., Kozlowski-Reilly A., Shan N.,  
RA Swearengen-Shahid S., Snider J., Strong J.T., Thompson J.J., Yeakum M.,  
RA Leonard S., Pearson C., Trani L., Radionenko M., Waligorski J.E.,  
RA Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P.,  
RA Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Spieth J., Bieri T.A.,  
RA Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A.,  
RA Shottland Y., Sinha P., Wohlmann P.E., Cook L.L., Hickenbotham M.T.,  
RA Eldred J., Williams D., Jones T.A., She X., Ciccarelli F.D.,  
RA Izaurralde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X.,  
RA McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C.,  
RA Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Furey T.S.,  
RA Miller W., Eichler E.B., Bork P., Suyama M., Torrents D.,  
RA Waterston R.H., Wilson R.K.;  
RT "Generation and annotation of the DNA sequences of human chromosomes 2  
RT and 4.";

DR	MIM; 605194; gene.
DR	MIM; 605376; phenotype.
DR	MIM; 608808; phenotype.
DR	GO; GO:0007368; P:determination of left/right symmetry; NAS.
DR	InterPro; IPR000742; EGF_3.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR013032; EGF_like_reg.
DR	Pfam; PF00008; EGF_1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; FALSE_NEG.
DR	PROSITE; PS50026; EGF_3; 1.
KW	Developmental protein_Disease mutation; EGF-like domain;
KW	Gastrulation; Glycoprotein; Polymorphism; Signal.
KW	Signal
FT	SIGNAL 1 25
FT	CHAIN 26 223
FT	
FT	DOMAIN 86 115
FT	CARBOHYD 52 52
FT	DISULFID 90 97
FT	DISULFID 91 103
FT	DISULFID 105 114
FT	VARIANT 78 78
FT	
FT	VARIANT 112 112
FT	
FT	
FT	
FT	VARIANT 189 189
FT	
FT	
FT	SEQUENCE 223 AA; 24612 MW; B52852A00ABCFIA3 CRC64;
FT	
QY	Query Match 99.4%; Score 1241; DB 1; Length 223;
DB	Best Local Similarity 99.6%; Pred. No. 7.7e-100;
DB	Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 MTRWHVRLFTVSALQIINLNSVQREKHNGRGCEVTKVATQKRQSLNWTSSHFGE 60
DB	1 MTRWHVRLFTVSALQIINLNSVQREKHNGRGCEVTKVATQKRQSLNWTSSHFGE 60
QY	61 VTGSAGWGPEEPLPSRAFGEGASAPRCRCRNGGTCVLGSCFCVCPAHFTGRICEHDORR 120
DB	61 VTGSAGWGPEEPLPSRAFGEGASAPRCRCRNGGTCVLGSCFCVCPAHFTGRICEHDORR 120
QY	121 SECGALEHGAWTLRACHLCRCIFGALHCLPLOTDPDCDKPKDFLAASHAHGPSAGAPSLLL 180
DB	121 SECGALEHGAWTLRACHLCRCIFGALHCLPLOTDPDCDKPKDFLAASHAHGPSAGAPSLLL 180
QY	181 LLPCALLHLRLRPDAHPRSLSVPVLQRERRPCRPGLGHRL 223
DB	181 LLPCALLHLRLRPDAHPRSLSVPVLQRERRPCRPGLGHRL 223
RESULT 2	
FCFL_MOUSE	STANDARD; PRT; 202 AA.
ID	-FCFL_MOUSE
AC	P97766; Q496U5; Q9JIB7;
DT	20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT	01-MAY-1997, sequence version 1.
DT	07-MAR-2006, entry version 30.
DE	Cryptic protein precursor.
GN	Name=Cfcll;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muroidea; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY,
RP	DEVELOPMENTAL STAGE, AND GLYCOSYLATION.
RC	STRAIN=129/Sv;
RX	MEDLINE=97178978; PubMed=9053319;
RT	Shen M.M., Wang H., Leder P.;
RT	"A differential display strategy identifies Cryptic, a novel EGF-



related gene expressed in the axial and lateral mesoderm during mouse gastrulation."

RT Development 124:429-442(1997).

RL [2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavanti T.L., Scheetz T.E.,

RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-154.

RX MEDLINE=20480687; PubMed=11024280; DOI=10.1016/S0378-1119(00)00337-1;

RA Colas J.-F., Schoenwolf G.C.,

RA Oszcelik C., Lankes W., Strehle M., Britsch S., Blum M.,

RA Birchmeier C.,

RT "A role of the cryptic gene in the correct establishment of the left-

RT right axis."

RL Curr. Biol. 9:1339-1342(1999).

CC -1- FUNCTION: Involved in the correct establishment of the left-right

CC axis. May play a role in mesoderm and/or neural patterning during

CC gastrulation.

CC -1- TISSUE SPECIFICITY: No expressed in adult tissues.

CC -1- DEVELOPMENTAL STAGE: Expressed during gastrulation (from 6.5 dpc

CC to 11 dpc) in two spatial domains that correspond to the axial and

CC lateral mesoderm. In the first domain expression is progressively

CC localized to the anterior primitive streak, the head process, and

CC the node and notochordal. In the second domain, expression is

CC initially concentrated in the lateral region of the egg cylinder,

CC and is later found circumferentially in the intermediate and

CC lateral plate mesoderm. Furthermore, the expression can also be

CC detected at the early head-fold stage in the midline

CC neuroectoderm, and consequently is an early marker for the

CC prospective floor plate of the neural tube. Expression ceases at

CC the end of gastrulation, and has not been observed in later

CC embryonic stages.

CC -1- PTM: N-glycosylated.

CC -1- MISCELLANEOUS: Mice lacking functional Cfc1 showed positional

CC defects in internal organs. The lung presents a right pulmonary

CC isomerism. The stomach is located on either the left or the right

CC and the spleen is small and has an abnormal shape. The apex of the

CC heart pointed to the right or left. In addition malpositioning of

CC heart outflow tracts is observed, the aorta is connected to the

CC right ventricle and emerged from the heart in a ventral position

CC and to the right of the pulmonary artery. This one is connected to

CC either the left or the right ventricle.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -----

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CC -----

CC EMBL; U57720; AAC53042.1; -; mRNA.

DR EMBL; BC100705; AA100706.1; -; mRNA.

DR EMBL; BC100706; AA100707.1; -; mRNA.

DR EMBL; BC100708; AA100709.1; -; mRNA.

DR EMBL; BC100711; AA100712.1; -; mRNA.

DR EMBL; AF242430; AAF76323.1; -; Genomic\_DNA.

DR HSSP; P00749; IURK.

DR Ensemble; ENSMUSG00000026124; Mus musculus.

DR MGI; MGI:109448; Cfc1.

DR GO; GO:0005615; C:extracellular space; TAS.

DR InterPro; IPR000742; EGF\_3.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR013032; EGF\_like\_reg.

DR Pfam; PF00008; EGF\_1.

DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.

DR PROSITE; PS50026; EGF\_3; 1.

DR Developmental protein; EGF-like domain; Gastrulation; Glycoprotein;

KW Signal.

KW SIGNAL 1 35 Potential

FT CHAIN 36 202 Cryptic protein.

FT DOMAIN 94 123 /FTID=PRO\_0000044631.

FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).

FT DISULFID 98 105 By similarity.

FT DISULFID 99 111 By similarity.

FT DISULFID 113 122 By similarity.

FT CONFLICT 83 83 P -> T (in Ref. 2; AA100707).

SQ SEQUENCE 202 AA; 21792 MW; 57035AD339A16FD7 CRC64;

Query Match 39.1%; Score 488; DB 1; Length 202;

Best Local Similarity 54.6%; Pred. No. 2.4e-34;

Matches 100; Conservative 16; Mismatches 65; Indels 2; Gaps 1;

QY 5 HHVRLFTVSLALQIILNGNSYQREKHNGRGVTKVATQKRSPLNWTSSHFGEVTS 64

DB 15 HQARPLFLVTVALQLGLGVSYQSE--GDGAREVSNILSPVIGTTLDRTLNSSRKNDI 72

QY 65 AEWGPEEPLPYSRATGEGASAPRCRNGGTGCVLGSFCVCPAHFTGRYCEHQRRECG 124

DB 73 PEGARLWDSLPSDSTLGSASVPVSRCHNGGTGCVLGSFCVCPAYFTGRYCEHQRREDCG 132

QY 125 ALEHGAWTLPACHLCRCIFCALHCLPLOTDRCDPKDFLASHAHGSPAGCAPSLLLLPLC 184

DB 133 ALGHGAWTLHSCRLCRCIFCALHCLPLOTDRCDPKDFLASHAHGSPAGCAPSLLLLPLC 192

QY 185 ALL 187

DB 193 LLL 195

RESULT 3

CCFC1\_CHICK

ID\_CFC1\_CHICK STANDARD; PRT; 193 AA.

AC Q918Q3; 2005, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2000, sequence version 1.

DT 07-MAR-2006, entry version 25.

DE Cryptic protein precursor (Cricpto-related factor 1).

GN Name=CFC1;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], FUNCTION, AND DEVELOPMENTAL

RP STAGE..

RX MEDLINE=20480687; PubMed=11024280; DOI=10.1016/S0378-1119(00)00337-1;

RA Colas J.-F., Schoenwolf G.C.,

RT "Subtractive hybridization identifies chick-cricpto, a novel EGF-CFC

RT ortholog expressed during gastrulation, neurulation and early  
 RT cardiogenesis.";  
 RL Gene 255:205-217 (2000).  
 RN [2]  
 RA NUCLEOTIDE SEQUENCE [MRNA].  
 RA Schlange T., Schnipkow I., Andree B., Ebert A., Zile M.H.,  
 RA Arnold H.-H., Brand T.;  
 RA "Dual function of chicken cryptic in the determination of left-right  
 RT asymmetry: control of midline barrier formation and lateralization of  
 RT the lateral plate mesoderm.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: May play a role in mesoderm and/or neural patterning  
 CC during gastrulation.  
 CC -1- DEVELOPMENTAL STAGE: First detected in the early-streak embryo,  
 CC specifically in the epiblast layer. At the late streak stage,  
 CC expression is condensed in the rostral half of the primitive  
 CC streak. At HH stage 4 expression appeared for the first time in  
 CC the mesodermal layer of the presumptive prechordal plate  
 CC rostrally and in the expanding mesoderm laterally. At HH stage 6,  
 CC labeling in mesodermal progenitors underlying the future  
 CC forebrain level of the neuraxis reached its maximum, whereas  
 CC mesoderm expression, which was restricted to the lateral plate,  
 CC was accompanied by an underlying endodermal expression at the  
 CC level of the heart-forming regions. Later gastrulation (HH stage  
 CC 5-7) was marked by strong expression in the notochord, beneath the  
 CC future floor plate of the neural tube. Expressed in Hensen's node,  
 CC within its mesenchymal core beneath the epiblast, and at a time  
 CC when it is morphologically asymmetric.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 DR EMBL; AF228760; AAF97868.1; -; mRNA.  
 DR EMBL; AF228762; AAF97869.1; -; Genomic DNA.  
 DR EMBL; AF228761; AAF97869.1; JOINED; Genomic DNA.  
 DR EMBL; AF228761; AAF97869.1; JOINED; Genomic DNA.  
 DR EMBL; AF228761; AAF97869.1; JOINED; Genomic DNA.  
 DR HSSP; P00749; 100K.  
 DR InterPro; ENSGALG0000012623; Gallus gallus.  
 DR InterPro; IPRO00742; EGF 3.  
 DR InterPro; IPRO06209; EGF-like.  
 DR InterPro; IPRO13032; EGF\_like\_reg.  
 DR Pfam; PF00008; EGF, 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR Developmental protein, EGF-like domain; Gastrulation; Glycoprotein;  
 KW Signal.  
 FT SIGNAL 1 25 Potential.  
 FT CHAIN 26 193 Cryptic protein.  
 FT /FTID=PRO\_0000044632.  
 FT DOMAIN 91 115 EGF-like.  
 FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 91 103 By similarity.  
 FT DISULFID 105 114 By similarity.  
 SQ SEQUENCE 193 AA; 23332 MW; B585A98F2D56325F CRC64;  
 Query Match 25.8%; Score 322.5; DB 1; Length 193;  
 Best Local Similarity 34.9%; Pred. No. 5.9e-20;  
 Matches 68; Conservative 34; Mismatches 76; Indels 17; Gaps 5;  
 QY 1 MTRVHVRLLFTVSLALQIINLNSVQREKHNGRGEVTKVATQKHQSPNNWTS----- 55  
 Db 1 MFWRKHVRLLFTVTLVQAIHLGKREHEK----DVKNFNDAQKQSPKNSVTIIDAF 56  
 QY 56 SHGEVTSAGNEGPPPELPYSRAFGEGASARPRCCNGGTCVLGSCFVCVCPAHTGRYCE 115  
 Db 57 SDMNQSYQGRKQKQNSREFVFT-GITESKNLNRCNCQNGTCTLGAFACPKRHFSGRHC 115  
 QY 116 HDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD---PKDFLASHAGPSA 172  
 Db 116 ----LRKCGSIHGDVWVGKWLRCCLYGLTKLCSQNTQDGCBLRREERIIRLYSNGRL 171

QY 173 GGAPSLLLLLPCALL 187  
 Db 172 QQTMSALICLLTFL 186  
 RESULT 4  
 Q50415 BRARE PRELIMINARY; PRT; 183 AA.  
 AC Q50415;  
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.  
 DT 07-JUN-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Oep protein.  
 GN Name:oep;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rosa S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smaluk D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP TISSUE=Embryo;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
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 CC  
 DR EMBL; BC095007; AAH95007.1; -; mRNA.  
 DR Ensembl; ENSDARG0000035095; Danio rerio.  
 DR ZFIN; ZDB-GENE-990415-198; oep.  
 DR InterPro; IPRO13032; EGF\_like\_reg.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN 1.  
 SQ SEQUENCE 183 AA; 20374 MW; 5571447894E18507 CRC64;  
 Query Match 22.9%; Score 286; DB 2; Length 183;  
 Best Local Similarity 43.0%; Pred. No. 8.4e-17;  
 Matches 52; Conservative 16; Mismatches 51; Indels 2; Gaps 2;  
 QY 71 EEPLPYSAFGEGASARPRCCNGGTCVLGSCFVCVCPAHTGRYCEHDSRSECGALEHGA 130  
 Db 65 EAALPFVGLTVAKQSR-TCCNGGTCILGSCFACPKYFGRSCYDERLDRDGVPHGE 123  
 QY 131 WTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGASLLLLLPCALLHRL 190  
 Db 124 WVKGCSYCRGCGYGLLHCFPHVFSKDCDDSQBVRHRSQ-SLRTLSSTIVMFAAFILHRL 182  
 QY 191 L<sub>1</sub>191

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Db 183 L 183
RESULT 5
O57517 BRARE PRELIMINARY; PRT; 183 AA.
ID O57517;
AC O57517;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE One-eyed pinhead short form protein.
GN Name=oeep;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98117252; PubMed=9458048; DOI=10.1016/S0092-8674(00)80918-6;
RA Zhang J., Talbot W.S., Schier A.F.;
RT "Positional cloning identifies zebrafish one-eyed pinhead as a
RT permissive EGF-related ligand required during gastrulation.";
RL Cell 92:241-251(1998).
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CC -----
Db 183 L 183
RESULT 6
O57516 BRARE PRELIMINARY; PRT; 190 AA.
ID O57516;
AC O57516;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE One-eyed pinhead long form protein.
GN Name=oeep;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98117252; PubMed=9458048; DOI=10.1016/S0092-8674(00)80918-6;
RA Zhang J., Talbot W.S., Schier A.F.;
RT "Positional cloning identifies zebrafish one-eyed pinhead as a
RT permissive EGF-related ligand required during gastrulation.";
RL Cell 92:241-251(1998).
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CC -----
Db 183 L 183
RESULT 7
O2VU94 XENLA PRELIMINARY; PRT; 179 AA.
ID O2VU94;
AC O2VU94;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 short transcript variant (cripto-3 short).
GN Name=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT Xenopus development.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
Db 183 L 183
Query Match 22.8%; Score 285; DB 2; Length 183;
Best Local Similarity 43.0%; Pred. No. 1e-16; Indels 2; Gaps 2;
Matches 52; Conservative 16; Mismatches 51;
QY 71 EEPYSAFEGASAPRCRNGTGVLCGFCVCPAHTGRCYCEHDSRSECGALEHGA 130
Db 65 EAALPFVGLTGVAQKSR-TCKNGGTGILGSCFACPKYFTGRSCYDELRDGVIPHGE 123
QY 131 WTLRACHLCRCIFGALHCLPDTFPCDPCDFLASHAHGPSAGASPSLLLLPCALLHRL 190
Db 124 WVQKGCYCRGCGYLLHCFPHVFSKDCDQSVRWRHSG-SLRTLSSTIVMFATFILHRL 182
QY 191 L 191
Db 183 L 183
RESULT 8
O57515 BRARE PRELIMINARY; PRT; 190 AA.
ID O57515;
AC O57515;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE One-eyed pinhead long form protein.
GN Name=oeep;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98117252; PubMed=9458048; DOI=10.1016/S0092-8674(00)80918-6;
RA Zhang J., Talbot W.S., Schier A.F.;
RT "Positional cloning identifies zebrafish one-eyed pinhead as a
RT permissive EGF-related ligand required during gastrulation.";
RL Cell 92:241-251(1998).
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CC -----
Db 183 L 183
Query Match 22.1%; Score 275.5; DB 2; Length 190;
Best Local Similarity 41.1%; Pred. No. 7.2e-16; Indels 11; Gaps 4;
Matches 53; Conservative 18; Mismatches 47;
QY 71 EEPYSAFEGASAPRCRNGTGVLCGFCVCPAHTGRCYCEHDSRSECGALEHGA 130
Db 65 EAALPFVGLTGVAQKSR-TCKNGGTGILGSCFACPKYFTGRSCYDELRDGVIPHGE 123
QY 131 WTLRACHLCRCIFGALHCLPDTFPCDPCDFLASHAHGPSAGASPSLLLLPCALLHRL 182
Db 124 WVQKGCYCRGCGYLLHCFPHVFSKDCDQSVRWRHSG-SLRTLSSTIVMF 181
QY 183 PCALLHRL 191
Db 182 ATFILHRL 190
RESULT 9
O2VU94 XENLA PRELIMINARY; PRT; 179 AA.
ID O2VU94;
AC O2VU94;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 short transcript variant (cripto-3 short).
GN Name=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT Xenopus development.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
Db 183 L 183
Query Match 21.5%; Score 269; DB 2; Length 179;
Best Local Similarity 35.1%; Pred. No. 2.5e-15; Indels 32; Gaps 8;
Matches 60; Conservative 21; Mismatches 58;
QY 1 MTRRHVRLFTVSLALQ-IINLGSYQREKINGGR-----GEVTKVATQKHOSPLN 52
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Db      1 MWV---LKLFLYLTVOLSAVIRLGT---PKQNGTMINAGSELSEDTYVQKLLHH----- 48
Qy      53 WTSHFGEVGTSAEGWGPPELPYSRAFGEGASARPRCCRNCGTCTVLGSCFVCVCPAHTGR 112
Db      49 --VDHAGKEKSSV-----ETIPFI-GLTKNHALDKHCCKNGGTCTVLGSCFACPKHYTKR 99
Qy      113 YCEHDORRECCGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCPDKPL 163
Db      100 YCELHVHNRKCGIVPHGWQVKKALCRCMYGTMHCFP---SGDCDAKDYV 147

RESULT 8
TDGF1_MOUSE
ID      TDGF1_MOUSE      STANDARD;      PRT;      171 AA.
AC      P51865;
DT      01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT      01-OCT-1996, sequence version 1.
DT      07-MAR-2006, entry version 40.
DE      Teratocarcinoma-derived growth factor precursor (Epidermal growth
GN      factor-like Cripto protein);
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6; TISSUE=Embryo;
RX      MEDLINE=94094736; PubMed=7916676;
RA      Dono R., Scalera L., Pacifico F., Acampora D., Persico M.G.,
RA      Simeone A.;
RT      "The murine cripto gene: expression during mesoderm induction and
RT      early heart morphogenesis.";
RL      Development 118:1157-1168(1993).
RN      [2]
RP      NUCLEOTIDE SEQUENCE OF 135-171.
RC      STRAIN=129/Sv;
RX      MEDLINE=96269599; PubMed=8661720; DOI=10.1007/s003359900100;
RA      Liguori G., Tucci M., Montuori N., Dono R., Lago C.T., Pacifico A.F.,
RA      Persico M.G.;
RT      "Characterization of the mouse Tdgf1 gene and Tdgf pseudogenes.";
RL      Mamm. Genome 7:344-348(1996).
CC      -!- FUNCTION: Could play a role in the determination of the epiblastic
CC      cells that subsequently give rise to the mesoderm.
CC      -!- TISSUE SPECIFICITY: Expressed at low level in specific organs of
CC      the adult animal such as spleen, heart, lung and brain. During
CC      gastrulation, expressed in the forming mesoderm. In later stages
CC      of the developing heart, expression is restricted to the truncus
CC      arteriosus.
CC      -!- DEVELOPMENTAL STAGE: First expressed prior to the onset of
CC      gastrulation (early streak stage), then continues throughout
CC      embryonic development.
CC      -!- SIMILARITY: Contains 1 EGF-like domain.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
DR      EMBL; M87321; AAA37459.1; -; mRNA.
DR      EMBL; X94083; CAA63827.1; -; Genomic_DNA.
DR      PIR; I49612; I49612.
DR      HSSP; P00740; 1EDM.
DR      MG1; MG1; 98658; Tdgf1.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
DR      GO; GO:0001763; P:branching morphogenesis; IDA.
DR      GO; GO:0030154; P:cell differentiation; TAS.
DR      GO; GO:0008595; P:determination of anterior/posterior axis, e...; IMP.
DR      GO; GO:0007507; P:heart development; IDA.
DR      GO; GO:0030335; P:positive regulation of cell migration; IDA.
DR      InterPro; IPR000742; EGF 3.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR013032; EGF_like_reg.
DR      Pfam; PF00008; EGF; 1.
DR      PROSITE; PS00022; EGF 1; 1.
DR      PROSITE; PS0026; EGF 3; 1.
KW      EGF-like domain; Glycoprotein; Growth factor; Signal.
FT      SIGNAL      1      17      Potential.
FT      CHAIN      18      171      Teratocarcinoma-derived growth factor.
FT      DOMAIN      62      91      EGF-like.
FT      CARBOHYD      63      63      N-linked (GlcNAc...) (Potential).
FT      DISULFID      66      73      By similarity.
FT      DISULFID      67      79      By similarity.
FT      DISULFID      81      90      By similarity.
FT      DISULFID      99      117      By similarity.
FT      DISULFID      112      133      By similarity.
FT      DISULFID      115      124      By similarity.
SQ      SEQUENCE      171 AA; 18754 MW; C52051AECDBS380 CRC64;

Query Match      21.4%; Score 267; DB 1; Length 171;
Best Local Similarity 37.8%; Pred. No. 3.5e-15;
Matches 56; Conservative 11; Mismatches 63; Indels 18; Gaps 3;

Qy      58 FGEVGT-----SARGWGPPELPYSRAF-----GEGASARPRCCRNCGTCTVLGSCF 103
Db      20 FGPVAGRDLAIRDNSIWQKEPAVRDRSFQFVPSVGIQNSKSLNKTCLNGGTCTILGSCF 79
Qy      104 VCPAHTGTYCEHDORRECCGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD----P 159
Db      80 ACPPSFYGRNCEHDVHKEHCGSILHGTWLPKCKSLCRCWHGQLHCLPFTFLPGCDGHVMD 139
Qy      160 KDFLASHAHGPSAGGAPSLLLLPALL 187
Db      140 QDLKASRTPCQTPSPVTTFTMLAGACFL 167

RESULT 9
Q3UZP8_MOUSE
ID      Q3UZP8_MOUSE      PRELIMINARY;      PRT;      171 AA.
AC      Q3UZP8;
DT      11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT      11-OCT-2005, sequence version 1.
DT      21-FEB-2006, entry version 8.
DE      6 days embryo whole body cDNA, RIKEN full-length enriched library,
DE      clone:5630400f13 product:teratocarcinoma-derived growth factor, full
DE      insert sequence.
GN      Name=Tdgf1;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Whole body;
RX      MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA      Carninci P., Hayashizaki Y.;
RT      "High-efficiency full-length cDNA cloning.";
RL      Methods Enzymol. 303:19-44(1999).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Whole body;
RX      PubMed16141072; DOI=10.1126/science.1112014;
RA      Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA      Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA      Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA      Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA      Ambesi-Impombato A., Adeweller R., Aturaliya R.N., Bailey T.L.,
RA      Bansal K.P., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA      Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA      Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA      di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA      Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA      Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

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RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Huninick L., Tacconi M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Mader M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,  
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamashita T., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kagashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RN [6]

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischnann W., Gaasterland T., Giesi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baresi G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Katsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Hashigaki K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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-----  
CC EMBL; AK133730; BA521807.1; -, mRNA.  
DR MGI; MGI:98658; Tdglf1.  
DR GO; GO:0005615; C:extracellular space; RCA.  
DR GO; GO:0019897; C:extrinsic to plasma membrane; IDA.  
DR GO; GO:0008595; P:determination of anterior/posterior axis, e. . .; IMP.  
DR InterPro; IPR00742; EGF\_3.  
DR InterPro; IPR013032; EGF\_like\_reg.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR Cell adhesion; EGF-like domain.  
KW SEQUENCE 171 AA; 18646 MW; C53400FDEBFB6380 CRC64;  
SQ

Query Match 21.2%; Score 265; DB 2; Length 171;  
Best Local Similarity 37.8%; Pred. NO. 5.3e-15;  
Matches 56; Conservative 11; Mismatches 63; Indels 18; Gaps 3;



ID	Q2VU96_XENLA	PRELIMINARY;	PRT;	191 AA.
AC	Q2VU96;			
DT	10-JAN-2006,	integrated into UniProtKB/TrEMBL.		
DT	10-JAN-2006,	sequence version 1.		
DT	07-FEB-2006,	entry version 3.		
DE	CR2.			
GN	Names=CR2;			
OS	Xenopus laevis	(African clawed frog).		
OC	Eukaryota;	Metazoa;	Chordata;	Cranialata;
OC	Amphibia;	Batrachia;	Anura;	Mesobatrachia;
OC	Xenopodinae;	Xenopus;	Xenopus.	
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	PubMed=16339189;	DOI=10.1242/dev.02188;		
RT	Onuma Y., Yeo C.Y.,	Whitman M.G.		
RT	"XCR2, one of three	Xenopus EGF-CFC genes,	has a distinct role in the	
RT	regulation of left-right	patterning."		
RT	Development 133:237-250	(2006).		
CC	-----			
CC	Copyrighted by the UniProt	Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the	Creative Commons Attribution-NoDerivs License		
CC	-----			
CC	EMBL: AY796186;	AA081596.1; -; mRNA.		
CC	SEQUENCE	191 AA; 21681 MW; 95E9920E40F95531 CRC64;		
CC	-----			
CC	Query Match	20.9%;	Score 261;	DB 2; Length 191;
CC	Best Local Similarity	52.4%;	Pred. NO. 1.3e-14;	
CC	Matches	43;	Conservative 12;	Mismatches 25; Indels 2; Gaps 2;
QY	90	CCRNGTCVLGSCVCPAHFTGRYCYBHDORRSCGA-LEHGAWTLRACHLCRCIFGALHC	148	
DB	90	CCNNGTCVLGSCVCPRYFTGRHCEYDERAKHCTAKIQHGDWIRKGRCLRCRCAYGVLHC	149	
QY	149	LPLQTPDRCDPKDFLASHAGP	170	
DB	150	F-VETQTDCEVEEHSAP	170	
RESULT 15				
ID	Q2UZ97_XENLA	PRELIMINARY;	PRT;	190 AA.
AC	Q2UZ97;			
DT	24-JAN-2006,	integrated into UniProtKB/TrEMBL.		
DT	24-JAN-2006,	sequence version 1.		
DT	07-FEB-2006,	entry version 2.		
DE	Cripto-1.			
GN	Names=CR1;			
OS	Xenopus laevis	(African clawed frog).		
OC	Eukaryota;	Metazoa;	Chordata;	Cranialata;
OC	Amphibia;	Batrachia;	Anura;	Mesobatrachia;
OC	Xenopodinae;	Xenopus;	Xenopus.	
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	Dorey K., Hill C.S.;			
RT	"Role of EGF-CFC family	members in Notch signalling during early		
RT	Xenopus development."			
RL	Submitted (NOV-2004)	to the EMBL/GenBank/DBJ databases.		
CC	-----			
CC	Copyrighted by the UniProt	Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the	Creative Commons Attribution-NoDerivs License		
CC	-----			
CC	EMBL: AJ864898;	CAI15752.1; -; mRNA.		
CC	SEQUENCE	190 AA; 21455 MW; F7C5E388CDBB05BA CRC64;		
CC	-----			
CC	Query Match	20.0%;	Score 249.5;	DB 2; Length 190;
CC	Best Local Similarity	39.1%;	Pred. NO. 1.3e-13;	
CC	Matches	43;	Conservative 18;	Mismatches 44; Indels 5; Gaps 3;
QY	52	NTTSSHFGEVTSAGBWGP----	BEPLDYSRAFEAGASAPRCRCNGTCTVLGSCVCPAH	108
DB	43	NTISQPLQDTINATHGKSPVKSAKTLFF-LGITDTSKLNARKCCQNGTCTFLGTCICPKQ	101	

Qy 109 FTGRYCEHDORRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158  
Db 102 FTGRHCEHERRPASCAGVPHGDMIRQGCLLCRCVSVGLHCFKPESED-CD 150

Search completed: September 7, 2006, 11:59:05  
Job time : 299 secs



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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:11:27 ; Search time 174 Seconds  
(without alignments)  
593.660 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 1249

Sequence: 1 MTRHHVRLFTVSLALQII.....PSVLQRPRPCGRPLGHRL 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:\*

- 1: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1249	100.0	223	4	US-10-665-602-2
2	1249	100.0	229	3	US-09-764-893-98
3	1249	100.0	229	3	US-09-764-881-101
4	1249	100.0	229	3	US-09-764-853-608
5	1249	100.0	229	3	US-09-764-898-269
6	1249	100.0	229	3	US-09-764-881-101
7	1249	100.0	229	4	US-10-073-865-98
8	1249	100.0	229	4	US-10-242-747-101
9	1242	99.4	231	3	US-09-764-898-198
10	1241	99.4	223	4	US-10-295-027-422
11	1241	99.4	223	4	US-10-295-027-1293
12	1241	99.4	223	4	US-10-264-237-2712
13	1241	99.4	223	5	US-10-940-431-4
14	1233	98.7	223	4	US-10-257-113-2
15	488	39.1	202	5	US-10-940-431-3
16	275.5	22.1	190	5	US-10-940-431-6
17	264	21.1	160	4	US-10-016-447-7
18	264	21.1	166	4	US-10-424-599-231675
19	256	20.5	171	5	US-10-940-431-1
20	249.5	20.0	190	5	US-10-940-431-5
21	248.5	19.9	190	4	US-10-016-447-4
22	238	19.1	360	4	US-10-390-566-7
23	238	19.1	367	4	US-10-390-566-6
24	233	18.7	129	4	US-10-390-566-4
25	233	18.7	139	4	US-10-390-566-3
26	233	18.7	174	4	US-10-665-602-7
27	233	18.7	188	4	US-10-241-220-58

28	233	18.7	188	4	US-10-388-578-6	Sequence 6, Appli
29	233	18.7	188	4	US-10-390-566-1	Sequence 1, Appli
30	233	18.7	188	4	US-10-362-597A-3	Sequence 3, Appli
31	233	18.7	188	4	US-10-362-597A-6	Sequence 6, Appli
32	233	18.7	188	4	US-10-362-597A-96	Sequence 96, Appli
33	233	18.7	188	4	US-10-407-481-3	Sequence 3, Appli
34	233	18.7	188	4	US-10-407-481-6	Sequence 6, Appli
35	233	18.7	188	4	US-10-407-481-96	Sequence 96, Appli
36	233	18.7	188	4	US-10-712-124-58	Sequence 58, Appli
37	233	18.7	188	4	US-10-693-538-1	Sequence 1, Appli
38	233	18.7	188	4	US-10-389-431-6	Sequence 6, Appli
39	233	18.7	188	4	US-10-816-476-3	Sequence 3, Appli
40	233	18.7	188	4	US-10-816-476-6	Sequence 6, Appli
41	233	18.7	188	4	US-10-816-476-96	Sequence 96, Appli
42	233	18.7	188	5	US-10-872-972-58	Sequence 58, Appli
43	233	18.7	188	5	US-10-872-991-58	Sequence 58, Appli
44	233	18.7	188	5	US-10-491-997-28	Sequence 28, Appli
45	233	18.7	188	5	US-10-940-431-2	Sequence 2, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-665-602-2

; Sequence 2, Application US/10665602

; Publication No. US20040086967A1

; GENERAL INFORMATION:

; APPLICANT: Melesner, Paul S.

; TITLE OF INVENTION: Human Cripitin Growth Factor

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/665,602

; FILING DATE: 22-Sep-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/393,023A

; FILING DATE: 09-SEP-1999

; APPLICATION NUMBER: US 08/471,371

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Marks, Michelle S.

; REGISTRATION NUMBER: 41,971

; REFERENCE/DOCKET NUMBER: PF2000D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 223 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-665-602-2

Query Match 100.0%; Score 1249; DB 4; Length 223;

Best Local Similarity 100.0%; Pred. No. 1.2e-103;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGGEVTKVATQKHRSPLNWTSSHFGE 60  
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Db 61 VTGSAEGWGPEEPLPYSRAFEGEGASARPCRCRNGGTCVLGSCFVCPAHTGTRYCEHDQRR 120  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
QY 181 LLPCALLHRLRPDAPAHPSLVPSVLOQRERPCGRPLGHLRL 223  
Db 181 LLPCALLHRLRPDAPAHPSLVPSVLOQRERPCGRPLGHLRL 223

## RESULT 2

US-09-764-893-98  
; Sequence 98, Application US/09764893  
; Publication No. US20020086330A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ209  
; CURRENT APPLICATION NUMBER: US/09/764,893  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 98  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-893-98

Query Match 100.0%; Score 1249; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.2e-103;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGGEVTKVATQKHRSPLNWTSSHFGE 60  
Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGGEVTKVATQKHRSPLNWTSSHFGE 66  
QY 61 VTGSAEGWGPEEPLPYSRAFEGEGASARPCRCRNGGTCVLGSCFVCPAHTGTRYCEHDQRR 120  
Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASARPCRCRNGGTCVLGSCFVCPAHTGTRYCEHDQRR 126  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186  
QY 181 LLPCALLHRLRPDAPAHPSLVPSVLOQRERPCGRPLGHLRL 223  
Db 187 LLPCALLHRLRPDAPAHPSLVPSVLOQRERPCGRPLGHLRL 229

## RESULT 3

US-09-764-881-101  
; Sequence 101, Application US/09764881  
; Publication No. US20020086821A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT207  
; CURRENT APPLICATION NUMBER: US/09/764,881

; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 101  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-881-101

Query Match 100.0%; Score 1249; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.2e-103;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGGEVTKVATQKHRSPLNWTSSHFGE 60  
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QY 61 VTGSAEGWGPEEPLPYSRAFEGEGASARPCRCRNGGTCVLGSCFVCPAHTGTRYCEHDQRR 120  
Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASARPCRCRNGGTCVLGSCFVCPAHTGTRYCEHDQRR 126  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186  
QY 181 LLPCALLHRLRPDAPAHPSLVPSVLOQRERPCGRPLGHLRL 223  
Db 187 LLPCALLHRLRPDAPAHPSLVPSVLOQRERPCGRPLGHLRL 229

## RESULT 4

US-09-764-853-608  
; Sequence 608, Application US/09764853  
; Patent No. US20020090672A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ206  
; CURRENT APPLICATION NUMBER: US/09/764,853  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 939  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 608  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-853-608

Query Match 100.0%; Score 1249; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.2e-103;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGGEVTKVATQKHRSPLNWTSSHFGE 60  
Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGGEVTKVATQKHRSPLNWTSSHFGE 66  
QY 61 VTGSAEGWGPEEPLPYSRAFEGEGASARPCRCRNGGTCVLGSCFVCPAHTGTRYCEHDQRR 120

Db 67 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 126  
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186  
Qy 181 LLPCALLHRLLRDPADAPAHPSLPSVLQRRRRCGRPGLGHRL 223  
Db 187 LLPCALLHRLLRDPADAPAHPSLPSVLQRRRRCGRPGLGHRL 229

## RESULT 5

US-09-764-898-269  
; Sequence 269, Application US/09764898  
; Patent No. US20020090673A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P201  
; CURRENT APPLICATION NUMBER: US/09/764,898  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 269  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-898-269

Query Match 100.0%; Score 1249; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.2e-103;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 60  
Db 7 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 66  
Qy 61 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
Db 67 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 126  
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186  
Qy 181 LLPCALLHRLLRDPADAPAHPSLPSVLQRRRRCGRPGLGHRL 223  
Db 187 LLPCALLHRLLRDPADAPAHPSLPSVLQRRRRCGRPGLGHRL 229

## RESULT 6

US-09-764-881-101  
; Sequence 101, Application US/09764881  
; Publication No. US20030125246A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P207  
; CURRENT APPLICATION NUMBER: US/09/764,881  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 101

; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-881-101

Query Match 100.0%; Score 1249; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.2e-103;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 60  
Db 7 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 66  
Qy 61 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
Db 67 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 126  
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186  
Qy 181 LLPCALLHRLLRDPADAPAHPSLPSVLQRRRRCGRPGLGHRL 223  
Db 187 LLPCALLHRLLRDPADAPAHPSLPSVLQRRRRCGRPGLGHRL 229

## RESULT 7

US-10-073-865-98  
; Sequence 98, Application US/10073865  
; Publication No. US20030044904A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P209C1  
; CURRENT APPLICATION NUMBER: US/10/073,865  
; CURRENT FILING DATE: 2002-02-14  
; Prior Application removed - See file wrapper or Palm  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 98  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: misc\_feature  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-073-865-98

Query Match 100.0%; Score 1249; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.2e-103;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 60  
Db 7 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 66  
Qy 61 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
Db 67 VTGSAEGWGPEEPLPYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 126  
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180



; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-422

Query Match 99.4%; Score 1241; DB 4; Length 223;
Best Local Similarity 99.6%; Pred. No. 6.1e-103;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATOKHQPSPLNWTSSHFGE 60
Db 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATOKHQPSPLNWTSSHFGE 60

Qy 61 VTSAEGWGPEEPLPYSRAFEGEGASAPRCRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120
Db 61 VTSAEGWGPEEPLPYSRAFEGEGASAPRCRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120

Qy 121 SECALHGHGAWTLRACHLCRCIFGALHCLPLQTPDRCDDPKDFLASHAHGSPAGAPSLLL 180
Db 121 SECALHGHGAWTLRACHLCRCIFGALHCLPLQTPDRCDDPKDFLASHAHGSPAGAPSLLL 180

Qy 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRPCGRPLGHLRL 223
Db 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRPCGRPLGHLRL 223

RESULT 11
US-10-295-027-1293
; Sequence 1293, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natesha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1293

Query Match 99.4%; Score 1241; DB 4; Length 223;
Best Local Similarity 99.6%; Pred. No. 6.1e-103;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATOKHQPSPLNWTSSHFGE 60
Db 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATOKHQPSPLNWTSSHFGE 60

Qy 61 VTSAEGWGPEEPLPYSRAFEGEGASAPRCRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120
Db 61 VTSAEGWGPEEPLPYSRAFEGEGASAPRCRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120

Qy 121 SECALHGHGAWTLRACHLCRCIFGALHCLPLQTPDRCDDPKDFLASHAHGSPAGAPSLLL 180
Db 121 SECALHGHGAWTLRACHLCRCIFGALHCLPLQTPDRCDDPKDFLASHAHGSPAGAPSLLL 180

Qy 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRPCGRPLGHLRL 223
Db 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRPCGRPLGHLRL 223

RESULT 12
US-10-264-237-2712
; Sequence 2712, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2712
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2712

Query Match 99.4%; Score 1241; DB 4; Length 223;
Best Local Similarity 99.6%; Pred. No. 6.1e-103;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATOKHQPSPLNWTSSHFGE 60
Db 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATOKHQPSPLNWTSSHFGE 60

Qy 61 VTSAEGWGPEEPLPYSRAFEGEGASAPRCRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120
Db 61 VTSAEGWGPEEPLPYSRAFEGEGASAPRCRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120

QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
QY 181 LLPCALLHRLRPDAPAHPSLPSVLQRRPCGRPGLGHRL 223  
Db 181 LLPCALLHRLRPDAPAHPSLPSVLQRRPCGRPGLGHRL 223

RESULT 13  
US-10-940-431-4  
; Sequence 4, Application US/10940431  
; Publication No. US20050208045A1  
; GENERAL INFORMATION:  
; APPLICANT: Vale, Wylie  
; APPLICANT: Harrison, Craig A.  
; APPLICANT: Gray, Peter C.  
; TITLE OF INVENTION: CRYPTO Antagonism of Activin and TGF-  
; TITLE OF INVENTION: Signaling  
; FILE REFERENCE: D6525  
; CURRENT APPLICATION NUMBER: US/10/940,431  
; PRIOR FILING DATE: 2004-09-14  
; PRIOR APPLICATION NUMBER: 60/503,046  
; PRIOR FILING DATE: 2003-09-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Macintosh OS 10  
; SEQ ID NO 4  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence of human Criptic protein  
US-10-940-431-4

Query Match 99.4%; Score 1241; DB 5; Length 223;  
Best Local Similarity 99.6%; Pred. No. 6.1e-103;  
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MTRHHVRLFTVSLALQIINLGNYSYQREKHNGRGVEVTKVATQKHQSPLNWTSSTHSGE 60  
Db 1 MTRHHVRLFTVSLALQIINLGNYSYQREKHNGRGVEVTKVATQKHQSPLNWTSSTHSGE 60  
QY 61 VTGSAEGWGPEEPLPYSRAFEGASAPRCRCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
Db 61 VTGSAEGWGPEEPLPYSRAFEGASAPRCRCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
QY 181 LLPCALLHRLRPDAPAHPSLPSVLQRRPCGRPGLGHRL 223  
Db 181 LLPCALLHRLRPDAPAHPSLPSVLQRRPCGRPGLGHRL 223

RESULT 14  
US-10-257-113-2  
; Sequence 2, Application US/10257113  
; Publication No. US20030207293A1  
; GENERAL INFORMATION:  
; APPLICANT: DUCKER, KLAUS  
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN  
; FILE REFERENCE: MERCK-2519  
; CURRENT APPLICATION NUMBER: US/10/257,113  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: EP 00107142.2  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 223  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-257-113-2  
Query Match 98.7%; Score 1233; DB 4; Length 223;  
Best Local Similarity 99.1%; Pred. No. 3.2e-102;  
Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MTRHHVRLFTVSLALQIINLGNYSYQREKHNGRGVEVTKVATQKHQSPLNWTSSTHSGE 60  
Db 1 MTRHHVRLFTVSLALQIINLGNYSYQREKHNGRGVEVTKVATQKHQSPLNWTSSTHSGE 60  
QY 61 VTGSAEGWGPEEPLPYSRAFEGASAPRCRCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
Db 61 VTGSAEGWGPEEPLPYSRAFEGASAPRCRCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180  
QY 181 LLPCALLHRLRPDAPAHPSLPSVLQRRPCGRPGLGHRL 223  
Db 181 LLPCALLHRLRPDAPAHPSLPSVLQRRPCGRPGLGHRL 223  
RESULT 15  
US-10-940-431-3  
; Sequence 3, Application US/10940431  
; Publication No. US20050208045A1  
; GENERAL INFORMATION:  
; APPLICANT: Vale, Wylie  
; APPLICANT: Harrison, Craig A.  
; APPLICANT: Gray, Peter C.  
; TITLE OF INVENTION: CRYPTO Antagonism of Activin and TGF-  
; TITLE OF INVENTION: Signaling  
; FILE REFERENCE: D6525  
; CURRENT APPLICATION NUMBER: US/10/940,431  
; CURRENT FILING DATE: 2004-09-14  
; PRIOR APPLICATION NUMBER: 60/503,046  
; PRIOR FILING DATE: 2003-09-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Macintosh OS 10  
; SEQ ID NO 3  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence of mouse Criptic protein  
US-10-940-431-3

Query Match 39.1%; Score 488; DB 5; Length 202;  
Best Local Similarity 54.6%; Pred. No. 1.6e-35;  
Matches 100; Conservative 16; Mismatches 65; Indels 2; Gaps 1;  
QY 5 HHVRLFTVSLALQIINLGNYSYQREKHNGRGVEVTKVATQKHQSPLNWTSSTHSGEVTGS 64  
Db 15 HOARPLFTVVALQLGLGYSQSE--GDGAREVSNILSPVPGTTLDRTLSNSRKNDI 72  
QY 65 AEGWGPEEPLPYSRAFEGASAPRCRCNGGTCVLGSCFVCPAHFTGRYCEHDQRRSECG 124  
Db 73 PEGARLWDSLPSSTLGSASVPVSRCHNGGTCVLGSCFVCPAYFTGRYCEHDQRRDCG 132  
QY 125 ALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 184  
Db 133 ALHGAWTLHSCRLCRLCIFSALYCLPHQTFSHCDLKSFLSSGARGSRCSIFSLLLLVLC 192  
QY 185 ALL 187  
Db 193 LLL 195

Search completed: September 7, 2006, 12:14:55  
Job time : 175 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:12:11 ; Search time 33 Seconds  
(without alignments)  
474.718 Million cell updates/sec

US-10-665-602-2

Perfect score: 1249

Sequence: 1 MTRHHVRLFTVSLALQII.....PSVLQRERRPCGRPLGHLRL 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications AA New:

- 1: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SID83/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	127.5	10.2	713	7	US-11-175-714-5
2	123	9.8	810	6	US-10-781-841-34
3	123	9.8	4391	7	US-11-183-325-56
4	121.5	9.7	2556	7	US-11-264-243-6
5	121	9.7	1198	7	US-11-217-997-14
6	120.5	9.6	720	7	US-11-175-714-4
7	120.5	9.6	2494	6	US-10-669-920-22
8	117.5	9.4	2505	6	US-10-669-920-15
9	117.5	9.4	5738	6	US-10-505-828-150
10	116	9.3	162	7	US-11-217-997-10
11	116	9.3	173	7	US-11-217-997-36
12	115.5	9.2	2556	7	US-11-071-796A-22
13	115	9.2	170	7	US-11-217-997-8
14	114.5	9.2	587	7	US-11-030-653-32
15	114.5	9.2	618	7	US-11-178-724-19
16	114.5	9.2	618	7	US-11-071-796A-18
17	114	9.1	324	6	US-10-669-920-906
18	114	9.1	2451	6	US-10-669-920-908
19	114	9.1	2503	6	US-10-539-328-723
20	111	8.9	723	7	US-11-178-724-18
21	111	8.9	723	7	US-11-071-796A-17
22	111	8.9	729	7	US-11-175-714-8
23	111	8.9	830	7	US-11-175-714-11
24	111	8.9	1953	7	US-11-264-243-16
25	110.5	8.8	1398	7	US-11-217-997-4

Sequence 6, Appli  
Sequence 5, Appli  
Sequence 22, Appli  
Sequence 21, Appli  
Sequence 38, Appli  
Sequence 30, Appli  
Sequence 27, Appli  
Sequence 12, Appli  
Sequence 2, Appli  
Sequence 22, Appli  
Sequence 16, Appli  
Sequence 20, Appli  
Sequence 18, Appli  
Sequence 40, Appli  
Sequence 40, Appli  
Sequence 3263, Ap  
Sequence 37, Appli  
Sequence 8, Appli  
Sequence 7, Appli  
Sequence 12, Appli

#### ALIGNMENTS

#### RESULT 1

US-11-175-714-5

Sequence 5, Application US/11175714

Publication No. US20060122373A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: McCarthy, Sean A.

APPLICANT: Gearing, David

APPLICANT: Holtzman, Douglas A.

APPLICANT: Pan, Yang

APPLICANT: Busfield, Samantha J.

APPLICANT: Barnes, Thomas M.

APPLICANT: Mackay, Charles

APPLICANT: Lora, Jose M.

TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,

TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: MPI05-0100NMIM

CURRENT APPLICATION NUMBER: US/11/175,714

CURRENT FILING DATE: 2005-07-05

PRIOR APPLICATION NUMBER: US 10/417,719

PRIOR FILING DATE: 2003-04-17

PRIOR APPLICATION NUMBER: US 09/568,218

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US 09/872,855

PRIOR FILING DATE: 1997-06-11

PRIOR APPLICATION NUMBER: US 09/832,633

PRIOR FILING DATE: 1997-04-04

PRIOR APPLICATION NUMBER: US 10/895,676

PRIOR FILING DATE: 2004-07-21

PRIOR APPLICATION NUMBER: US 10/105,934

PRIOR FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: US 09/862,972

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 09/062,389

PRIOR FILING DATE: 1998-04-17

PRIOR APPLICATION NUMBER: US 60/062,017

PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: US 60/044,746

PRIOR FILING DATE: 1997-04-18

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 195

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 713

TYPE: PRT

ORGANISM: Rattus Norvegicus

US-11-175-714-5

Query Match 10.2%; Score 127.5; DB 7; Length 713;  
Best Local Similarity 25.3%; Pred. No. 0.00074;  
Matches 55; Conservative 11; Mismatches 70; Indels 81; Gaps 9;

Qy 20 INLGNYSQREKHNGGRGEVTKVATQKHRSQPLNWTSSHFGVETGSAEGWGPPEPLPYSRA 79  
Db 419 VDLGNSYLRCQTCQFSGRYCEDNVDDCASSP----- 449

Qy 80 FEGASARPRCCRRNGGTC---VLGSFVCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRAC 136  
Db 450 -----CANGGTCRSDVNDFSCTCPGYTGKNCAPVSRCEHAPCHNGA---TC 494

Qy 137 H-----LCRCI---FGALHC---LPLQTPRCDPKDFLASHAHGPS-----AGGAPSL 178  
Db 495 HORGQRYMCECAQGYGANCQFLLPPEPPD-----LIVAAQGGSPFWAVACAGVVLVL 547

Qy 179 LLLLPCALLHRLRPDAPAHPRSLVPSVLQRRRRPCG 215  
Db 548 LLLGCAAVVVCVRLKLQKH-----QPPDPDCG 575

## RESULT 2

US-10-781-841-34  
; Sequence 34, Application US/10781841  
; Publication No. US20060134634A1  
; GENERAL INFORMATION:  
; APPLICANT: FUJIWARA, TSUTOMU  
; APPLICANT: WATANABE, TAKESHI  
; APPLICANT: HORIE, MASATO  
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN  
; FILE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME  
; FILE REFERENCE: Q-53599  
; CURRENT APPLICATION NUMBER: US/10/781.841  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: US/10/342,276  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US/09/976,165  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/565,538  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 09/055,699  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: 08/820,170  
; PRIOR FILING DATE: 1997-03-19  
; PRIOR APPLICATION NUMBER: JP 63410/1996  
; PRIOR FILING DATE: 1996-03-19  
; PRIOR APPLICATION NUMBER: JP 69163/1997  
; PRIOR FILING DATE: 1997-03-05  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 810  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-781-841-34

Query Match 9.8%; Score 123; DB 6; Length 810;  
Best Local Similarity 40.5%; Pred. No. 0.0022;  
Matches 30; Conservative 5; Mismatches 25; Indels 14; Gaps 4;

Qy 81 GEGASARPRC---CRNGTCVLGSFVCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACH 137  
Db 510 GNGTICRAFCEGCRYGGTCVAPNKCVCPSGFTGSHCEKIDECSEGIIE-----CH 561

Qy 138 -LCRCIF--GALHC 148  
Db 562 NHRRCVNLPGWYHC 575

## RESULT 3

US-11-183-325-56  
; Sequence 56, Application US/11183325

Publication No. US20060104898A1  
; GENERAL INFORMATION:  
; APPLICANT: Vanderbilt University  
; APPLICANT: Hallahan, Dennis E  
; APPLICANT: Ou, Shinnian  
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES  
; FILE REFERENCE: 1242/47/2/2 CIP  
; CURRENT APPLICATION NUMBER: US/11/183,325  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 60/328123  
; PRIOR FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: US 10/259,087  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 56  
; LENGTH: 4391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: P98160  
; DATABASE ENTRY DATE: 2003-02-28  
; RELEVANT RESIDUES: (1)..(4391)  
US-11-183-325-56

Query Match 9.8%; Score 123; DB 7; Length 4391;  
Best Local Similarity 27.3%; Pred. No. 0.013;  
Matches 39; Conservative 4; Mismatches 42; Indels 58; Gaps 4;

Qy 85 SARPPCCRRNGGTC---VLGSFVCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCR 140  
Db 3847 TCRDRPCCQGGQCHDSSESSYVCVCPAGFTGRCEHSQ----- 3884

Qy 141 CIFGALHCLPLQTPRCDPKDFLASHAHG-----PSAGGAP 176  
Db 3885 ----ALHC---HPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCBEGVTVTTTSLSGAG 3936

Qy 177 SLLLLPCALLHRLRLRPDAPAH 199  
Db 3937 SYLALPALNTTHLERLDVEFKP 3959

## RESULT 4

US-11-264-243-6  
; Sequence 6, Application US/11264243  
; Publication No. US20060134121A1  
; GENERAL INFORMATION:  
; APPLICANT: Thurston, Gavin  
; APPLICANT: Gale, Nicholas  
; APPLICANT: Noguera, Irene  
; TITLE OF INVENTION: DLL4 Antagonists, Assays and Therapeutic  
; FILE REFERENCE: 2070A  
; CURRENT APPLICATION NUMBER: US/11/264,243  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: 60/623,658  
; PRIOR FILING DATE: 2004-10-29  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 2556  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-11-264-243-6

Query Match 9.7%; Score 121.5; DB 7; Length 2556;  
Best Local Similarity 30.5%; Pred. No. 0.0099;  
Matches 46; Conservative 10; Mismatches 62; Indels 33; Gaps 9;

Qy 88 PRC----CRNGGTCV--LGSP-CVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCR 140  
Db 986 PDCTESSCFNGGTCVDGINSFTCLCPGFTGSGYQCQHDVNECDSPCLHGGTCQDGGCGSVR 1045



Qy 141 CIGFALHCLPLQTPDRCDPKDFLASHAHGFSAGGASLLLLLPALLHRLRLPDAPAPHR 200  
Db 1046 CT-----CPQYTGPN-C-QNLVHWCDSPPCKNGG-----KCMQHTQVRCPCPSGT 1091  
Qy 201 SL-----VPSV-----LQRE-----RRPCGRPGL 219  
Db 1092 GLYCDVPSVEVAARQGVQDVVARLCQHGGL 1122

RESULT 5  
US-11-217-997-14  
; Sequence 14, Application US/11217997  
; Publication No. US20060111561A1  
; GENERAL INFORMATION:  
; APPLICANT: Valerie L. Gerlach  
; APPLICANT: Elma R. Fernandes  
; APPLICANT: Richard A. Shinkets  
; APPLICANT: Meera Patturajan  
; APPLICANT: Vladimir Y. Gusev  
; APPLICANT: Stacie (Casman) Navara  
; APPLICANT: Velizar T. Tchernev  
; APPLICANT: David W. Anderson  
; APPLICANT: XiaoJia (Sasha) Guo  
; APPLICANT: Luca Rastelli  
; APPLICANT: Mei Zhong  
; APPLICANT: Muralidhara Padigaru  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY  
; FILE REFERENCE: Cura 551 CIP  
; CURRENT APPLICATION NUMBER: US/11/217,997  
; CURRENT FILING DATE: 2005-08-31  
; PRIOR APPLICATION NUMBER: 10/453,372  
; PRIOR FILING DATE: 2003-06-03  
; PRIOR APPLICATION NUMBER: 10/055,877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,478  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/263,351  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/272,870  
; PRIOR FILING DATE: 2001-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 14  
; LENGTH: 1198  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-217-997-14

Query Match 9.7%; Score 121; DB 7; Length 1198;  
Best Local Similarity 30.0%; Pred. No. 0.005;  
Matches 48; Conservative 14; Mismatches 56; Indels 42; Gaps 10;  
Qy 83 GASAPRC-CRNGTCC-VLGSFCVCPAHFTGTRYCEHD-----QRRSEC-----GALEHGAWT 132  
Db 992 GDCNRHSCLCQNGCTDPVSGHCAPCEGWAGLACECPDRVAGCRHSGGCLNGG--- 1048  
Qy 133 LRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGASLLLL----- 181  
Db 1049 LCDPHTGRCL-----CPAGWTGDKCQ-----SHPHGLLEASAAIFLPACGAGLERP 1097  
Qy 182 LPCALLHRLRLP-----DAPAHPRSLVPSVLQRRPCG 215

Db 1098 VPSAAAAARLPLPATTSLGPAAPVPLASLAPAA-SRDVRPGG 1136

RESULT 6  
US-11-175-714-4  
; Sequence 4, Application US/11175714  
; Publication No. US20060122373A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Gearing, David  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Pan, Yang  
; APPLICANT: Busfield, Samantha J.  
; APPLICANT: Barnes, Thomas M.  
; APPLICANT: Mackay, Charles  
; APPLICANT: Lora, Jose M.  
; TITLE OF INVENTION: DELTA3, FTMA-070, TANGO85, TANGO77,  
; TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN  
; FILE REFERENCE: MPI05-010OMNIM  
; CURRENT APPLICATION NUMBER: US/11/175,714  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 10/417,719  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US 09/568,218  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 09/872,855  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: US 09/832,633  
; PRIOR FILING DATE: 1997-04-04  
; PRIOR APPLICATION NUMBER: US 10/895,676  
; PRIOR FILING DATE: 2004-07-21  
; PRIOR APPLICATION NUMBER: US 10/105,934  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: US 09/862,972  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 09/062,389  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: US 60/062,017  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/044,746  
; PRIOR FILING DATE: 1997-04-18  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 720  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-11-175-714-4

Query Match 9.6%; Score 120.5; DB 7; Length 720;  
Best Local Similarity 30.0%; Pred. No. 0.0033;  
Matches 45; Conservative 8; Mismatches 56; Indels 41; Gaps 8;  
Qy 91 CRNGTCC---VLGSFCVCPAHFTGTRYCEHDORSECCALEHGAWTLRACH-----LCRC 141  
Db 449 CANGGTCDSDVDFSCCTPGPYTGKNCSPVSRCEHAPCHNGA-----TCHQRGQRYMCEC 504  
Qy 142 I--FGALHC---LPLQTPDRCDPKDFLASHAHGFSAGG-----APSLLLLLLPCA 185  
Db 505 AQYGGNCCOFLPEPPP---GPMVVDLSERHMSQGGPPFWAVCAVGVVLVLLLLGCA 561  
Qy 186 LHLRLRPDAPAHPRSLVPSVLQRRPCG 215  
Db 562 AVVVCVRLKLQKH-----QPPPEPCG 582  
RESULT 7  
US-10-669-920-22  
; Sequence 22, Application US/10669920  
; Publication No. US20060194265A1

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; SEQ ID NO 15
; LENGTH: 2505
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-15

Query Match          9.4%; Score 117.5; DB 6; Length 2505;
Best Local Similarity 29.4%; Pred. No. 0.023;
Matches 40; Conservative 12; Mismatches 57; Indels 27; Gaps 8;

QY      87 RPRCCRNGGTCVLG---SFCVCPAHFTGRYCEHDDRRSECGALEHGAWTLRAC---HLCLR 140
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB      900 RPNPCHNGSGCTDGINATAFCDCLPGFQGAFCEED--INECNPCQNGA-NCTDCVDSTYCT 956

QY     141 CI--FGALHCLPLQTDPDRCKPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDPAHAH 198
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB     957 CPVGFGIHC-ENNTPTDCTESSCFNG---GTCVDGINSFTCLCPGFTGSYCQYD---- 1007

QY     199 PRSLVPSVLQRERRPC 214
       |::|:|
DB    1008 -----VNECDSRPC 1016

RESULT 9
US-10-505-928-150
; Sequence 150, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 150
; LENGTH: 5738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-150

Query Match          9.4%; Score 117.5; DB 6; Length 5738;
Best Local Similarity 26.6%; Pred. No. 0.053;
Matches 55; Conservative 6; Mismatches 65; Indels 81; Gaps 11;

QY     59 GEVTGSAEWGPEEPLPY-SRAFGEGASARPCRNGGTGCVLSGFC-----VC---P 106
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB    3629 GSVFPG-AGGWGPWGFWSHCSRSCGGGLRSRTRACDQPPPOGLGDYCEGPPRAQGEVCOALP 3687

QY     107 AHFTGRYCEHDQRSSECGA-----LEHGAWTLRACHLCRCIFGALHCLPLQT----- 153
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB    3688 CPTNCTAIEGAESYSPGPPCRPCSDDLVHCVM-----RCQPGC-YCPPQQVLLSSNG 3738

QY     154 -----PDRCDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDPAHAHPSLVSLVQL 208
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB    3739 AICVPQGHCSCLDLLTGQRHHPGA-----RLARPDCGNHTCTL----- 3776

QY     209 RERR-----PCGRP 217
       |||:|||
DB    3777 -EGRLNCTDLPDCDGGGQSILHPGQP 3802

RESULT 10
US-11-217-997-10
; Sequence 10, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shimkets
; APPLICANT: Meera Patturajan
```

```
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-10

Query Match          9.3%; Score 116; DB 7; Length 162;
Best Local Similarity 28.6%; Pred. No. 0.0018;
Matches 42; Conservative 14; Mismatches 41; Indels 50; Gaps 10;

QY 61 VTGSAEGWGP-----EEPLPSYRAFGEASARPRC-CRNGGTC-VLGSFCVCPAFTG 111
Db 30 IPASARTEGPVTLQACEHPGPPG---FHGAGCGGLCWCQHGAPCDPISGRCLCPAGFHG 86
QY 112 RYCEHDDRSECCGALEHGAWTLRACHL-CRC-----IFGALHCL-----P 150
Db 87 HFCERDCRGQGP-----SCTLHDCGGGADCDPVSGQCHCVDGVMGTCTREGGP 137
QY 151 LQTPDRCDPKDFLASHAHGPSAGGAPS 177
Db 138 LRLPEN-----PSLAQG-SAGTLPA 156

RESULT 11
US-11-217-997-36
; Sequence 36, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shimkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
```

```
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 36
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-36

Query Match          9.3%; Score 116; DB 7; Length 173;
Best Local Similarity 28.6%; Pred. No. 0.0019;
Matches 42; Conservative 14; Mismatches 41; Indels 50; Gaps 10;

QY 61 VTGSAEGWGP-----EEPLPSYRAFGEASARPRC-CRNGGTC-VLGSFCVCPAFTG 111
Db 39 IPASARTEGPVTLQACEHPGPPG---FHGAGCGGLCWCQHGAPCDPISGRCLCPAGFHG 95
QY 112 RYCEHDDRSECCGALEHGAWTLRACHL-CRC-----IFGALHCL-----P 150
Db 96 HFCERDCRGQGP-----SCTLHDCGGGADCDPVSGQCHCVDGVMGTCTREGGP 146
QY 151 LQTPDRCDPKDFLASHAHGPSAGGAPS 177
Db 147 LRLPEN-----PSLAQG-SAGTLPA 165

RESULT 12
US-11-071-796A-22
; Sequence 22, Application US/11071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE BROCOLE
; APPLICANT: DALLMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
```

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; SEQ ID NO 22
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (891)
; OTHER INFORMATION: Variable amino acid
US-11-071-796A-22

Query Match          9.2%; Score 115.5; DB 7; Length 2556;
Best Local Similarity 35.6%; Pred. No. 0.035;
Matches 3; Conservative 6; Mismatches 34; Indels 27; Gaps 7;

Qy      83 GASARPRCCRRGGTGVCL-----GSFCVCPAHFTGRYCEHDQRKSECGALEHGAWTLRAC 136
Db      1311 GCKGKP--CKNGGTCAVASNTARGFICKPAGPEGATCENDAR--TCG-----SURCL 1359
           :|:||||:|
Qy      137 HLCRCIFG----ALHCLPLQTDRCDPKDFLASHAHGPSAGGAP 176
Db      1360 NGGTCTISGRSPSTCLCLGPETGPPEC---QPAS---SFLCLGNP 1397
           :|||:|||

RESULT 13
US-11-217-997-8
; Sequence 8, Application US/11217997
; Publication NO. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shinkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchervnev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; PRIOR FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 8
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-8
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:15:10 ; Search time 191 Seconds  
(without alignments)  
533.818 Million cell updates

Title: US-10-665-602-2  
 perfect score: 223  
 Sequence: 1 MTWRHHVRLLETYSVALQII.....PSVLQRRPPCGPGLGHL 223

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 30

Total number of hits satisfying chosen parameters: 15

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

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1: Geneseqp1980s.*
2: Geneseqp1930s.*
3: Geneseqp2000s.*
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5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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2	223	100.0	229	4	AAU18122	Novel hum	
3	223	100.0	229	4	AAU17028	Human nov	
4	223	100.0	229	4	AB10300	Human cDN	
5	223	100.0	229	4	ABU19904	Novel hum	
6	223	100.0	229	5	ABJ05749	Novel hum	
7	223	100.0	229	5	AB966887	Human pol	
8	187	83.9	223	6	AB900336	Human pol	
9	187	83.9	223	5	ABU56711	Lung canc	
10	187	83.9	223	7	ADN39104	Cancer/an	
11	187	83.9	223	7	ADN39975	Cancer/an	
12	187	83.9	223	9	ADY85563	Human cri	
13	187	83.9	231	4	AAU16957	Human nov	
14	149	66.8	230	2	AAW09111	Human cri	
15	145	65.0	223	5	AAG77914	Human cri	

## ALIGNMENTS

RESULT 1  
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ID ADO05060 standard; protein: 223 AA.

[illegible]

DE	Novel human uterine motility-association polypeptide #29.		
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KW	Human; uterine motility-association disorder; uterus; pregnancy; labour;	PR	21-SEP-2000; 2000US-0234223P.
KW	menstrual cycle; gene therapy.	PR	21-SEP-2000; 2000US-0234274P.
XX		PR	25-SEP-2000; 2000US-0234997P.
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XX		PR	27-SEP-2000; 2000US-0235836P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488777/53.
XX
XX N-PSDB; AAS28964.
XX
XX New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 11; SEQ ID NO 98; 524pp; English.
XX
XX The present invention relates to the isolation of novel human uterine
CC motility-association polypeptides, and cDNA (AAS28936-AAS28994) and
CC genomic sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with uterine motility such as pregnancy
CC and labour, and menstrual disorders. The polynucleotide sequences of the
CC invention are also useful in gene therapy. AAU18094-AAU18152 represent
CC novel human uterine motility-association polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 229 AA;
SQ
Query Match 100.0%; Score 223; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-195;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKHSPLNWTSSHFE 60
DB 7 MTRWHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKHSPLNWTSSHFE 66
QY 61 VTSAEGWGPEEPLPYSRAGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQR 120
DB 67 VTSAEGWGPEEPLPYSRAGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQR 126
QY 121 SECCALHGHAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSLLL 180
DB 127 SECCALHGHAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSLLL 186
QY 181 LLPCALLHRLLRDPADAPHRSLVPSVLQRRRPPCGRFGGLGHLR 223
DB 187 LLPCALLHRLLRDPADAPHRSLVPSVLQRRRPPCGRFGGLGHLR 229
RESULT 3
AAU17028
ID AAU17028 standard; protein; 229 AA.
XX
XX AAU17028;
AC
XX
XX 07-NOV-2001 (first entry)
DT
XX
XX Human novel secreted protein, SEQ ID 269.
DE
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
XX Homo sapiens.
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 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX

PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-476222/51.  
 DR N-PSDB; AAS26933.  
 XX  
 PT Novel polypeptides and polynucleotides useful as diagnostic reagents to  
 diagnose diseases or disorders associated with aberrant expression or  
 activity of polypeptides, for treating blood clotting disorder,  
 PT hemophilia.  
 XX  
 PS Claim 11; SEQ ID NO 269; 601pp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules and their  
 encoded secreted proteins. The nucleic acids and proteins are used to  
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Antibodies to the proteins can also be used in  
 CC alleviating symptoms associated with the disorders and in diagnostic  
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays  
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
 CC and many other disorders listed in the specification. The polypeptides  
 CC can also be used to aid wound healing and epithelial cell proliferation,  
 CC to prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence represents a novel secreted protein of the invention. Note: The  
 Query Match 100.0%; Score 223; DB 4; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-195;  
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 AC ABB10300;  
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 DT 10-JAN-2002 (first entry)  
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 XX  
 KW Human; gene therapy; neural disorder; immune system disorder;  
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
 KW pulmonary disorder; cardiovascular disorder; renal disorder;  
 KW proliferative disorder; inflammation.  
 XX  
 OS Homo sapiens.

XX WO200154474-A2.  
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XX 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251859P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-02559678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465568/50.
XX
XX N-PSDB; AAS31589.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; SEQ ID NO 101; 542bp; English.
XX
XX The present invention relates to the isolation of novel human calcium-
XX binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences
XX encoding for these proteins. The sequences of the invention are useful in
XX the diagnosis, prevention and/or prognosis of diseases associated with
XX aberrant calcium flux. Such disorders include neurological diseases (e.g.
XX amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe
CC combined immunodeficiency, SCID), digestive disorders (e.g. irritable
CC bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders
CC (e.g. haemophilia), and/or infectious disease (e.g. acquired
CC immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are
CC also useful as screening tools to identify antagonists and/or agonists
CC that may enhance or inhibit activities mediated by calcium-binding
CC proteins. The polynucleotides of the invention are also useful in gene
CC therapy. AAU19892-AAU1969 represent the novel human calcium-binding
CC proteins. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 229 AA;
XX
XX Query Match 100.0%; Score 223; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-195;
XX Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTWRHVRLLFTVSLALQIINLGNISYOREKHNGRGEVTKVATQKHRSPLNWTSSHFGE 60
DB 7 MTWRHVRLLFTVSLALQIINLGNISYOREKHNGRGEVTKVATQKHRSPLNWTSSHFGE 66
QY 61 VTGSAGWGPEEPLPYSRAFGEASAPRCRCRNGGTCVLGSCVCPAHFTGRVCEHQR 120
DB 67 VTGSAGWGPEEPLPYSRAFGEASAPRCRCRNGGTCVLGSCVCPAHFTGRVCEHQR 126
QY 121 SEGGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSL 180
DB 127 SEGGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSL 186
QY 181 LLPCALLHRLLRDPAPAHPRSLVPSVLQRRRRCGRPGLGHLRL 223
DB 187 LLPCALLHRLLRDPAPAHPRSLVPSVLQRRRRCGRPGLGHLRL 229
RESULT 6
ABJ05749
ID ABJ05749 standard; protein; 229 AA.
XX
XX AC ABJ05749;
XX
XX 14-NOV-2002 (first entry)
XX
XX Novel human protein SEQ ID No 98.
XX
XX Immunostimulant; antirheumatic; antiarthritic; neuroprotective;
XX anti-allergic; antidiabetic; antiaschmatic; antiinflammatory; nootropic;
XX immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic;
XX cytostatic; nephrotropic; antiparkinsonian; gynecological; virucide;
XX antibacterial; antiarrhythmic; fungicide; HCFAT05; HWAAB95; HTNBM01;
XX immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular;
XX inflammatory condition; graft-versus-host disease; reproductive system;
XX blood-related disorder; hyperproliferative; endocrine; neurological;
XX respiratory; renal; infectious disease; gastrointestinal; gene therapy;
XX neuronal growth; neuronal disorder; neuro-degenerative condition;
XX keratinocyte growth; human.
XX
XX OS Homo sapiens.
XX
XX XX US2002086330-A1.
XX
XX PD 04-JUL-2002.
XX
XX PF 17-JAN-2001; 2001US-00764893.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
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PR 26-JUL-2000; 2000US-0220963P.  
PR 28-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225477P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
XX  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
XX  
XX WPI; 2002-665432/71.  
DR  
XX  
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and  
PT treatment of immune, hyperproliferative, renal, respiratory,  
PT cardiovascular, reproductive, endocrine, gastrointestinal and  
PT neurological disorders.  
XX  
PS Disclosure; Page 268-269; 335pp; English.  
XX  
XX The invention relates to an isolated polypeptide comprising a sequence at  
CC least 90% identical to a full length protein sequence selected from 55  
CC sequences given in the specification such as a sequence of 163, 74 or 140  
CC amino acids fully defined in the specification, or the encoding sequence  
CC contained in 49 cDNA clones given in specification e.g. HCFAR05, HMAAE95  
CC or HTNBM01. The protein and its encoding nucleic acid are useful for  
CC diagnosing a pathological condition or susceptibility to a pathological  
CC condition in a subject and for preventing, treating or ameliorating a  
CC medical condition. The protein, its encoding nucleic acid and an isolated  
CC antibody that can bind to the protein are useful in treating, preventing,  
CC diagnosing and/or prognosing immunodeficiencies, autoimmune disorders,  
CC allergic reactions and conditions, inflammatory conditions, graft-versus-  
CC host disease, blood-related disorders, hyperproliferative disorders,  
CC renal disorders, cardiovascular disorders, respiratory disorders,  
CC neurological disorders, endocrine disorders, reproductive system

CC disorders, infectious diseases, and gastrointestinal disorders. The  
CC protein of the invention is useful to stimulate neuronal growth and to  
CC treat, prevent, and/or diagnose neuronal damage which occurs in certain  
CC neuronal disorders or neuro-degenerative conditions, for stimulating  
CC keratinocyte growth, to prevent hair loss, to modulate mammalian  
CC characteristics such as body height, weight, hair color, and to increase  
CC or decrease storage capabilities, fat content, lipid, protein,  
CC carbohydrate, vitamins, minerals, cofactors or other nutritional  
CC components. The nucleic acid of the invention can be used in gene  
CC therapy. This sequence represents a novel human protein of the invention  
XX  
SQ Sequence 229 AA;  
Query Match 100.0%; Score 223; DB 5; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.5e-195; Indels 0; Gaps 0;  
Matches 223; Conservative 0; Mismatches 0;  
QY 1 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGVTKVATQKHQSPLNWTSHPGE 60  
Db 7 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGVTKVATQKHQSPLNWTSHPGE 66  
QY 61 VTGSAEGWGPEPLPYSRAPFEGEGASAPRCRNGGTCTVLGSCVCPAHTGTCYCEHDQRR 120  
Db 67 VTGSAEGWGPEPLPYSRAPFEGEGASAPRCRNGGTCTVLGSCVCPAHTGTCYCEHDQRR 126  
QY 121 SECGALEHGCAWTLRACHLCRCIFGALHCLPLOTDPKDFLASHAHGSPAGAPSLLL 180  
Db 127 SECGALEHGCAWTLRACHLCRCIFGALHCLPLOTDPKDFLASHAHGSPAGAPSLLL 186  
QY 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCCGPGGLGHRL 223  
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCCGPGGLGHRL 229  
RESULT 7  
ABP66887  
ID ABP66887 standard; protein; 229 AA.  
XX  
AC ABP66887;  
XX  
XX 09-DEC-2002 (first entry)  
XX  
XX Human polypeptide SEQ ID NO 608.  
XX  
XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antisickling; antianemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX US2002090672-A1.  
XX  
XX 11-JUL-2002.  
PD  
XX 17-JAN-2001; 2001US-00764853.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225267P.







PR	29-NOV-2001; 2001US-0334393P.	ADN39975	
PR	03-DEC-2001; 2001US-0335394P.	ID	ADN39975 standard; protein; 223 AA.
PR	14-DEC-2001; 2001US-0340376P.	XX	
PR	08-JAN-2002; 2002US-0347211P.	AC	ADN39975;
PR	10-JAN-2002; 2002US-0347349P.	XX	
PR	08-FEB-2002; 2002US-0355250P.	DT	17-JUN-2004 (first entry)
PR	13-FEB-2002; 2002US-0356714P.	XX	
PR	20-FEB-2002; 2002US-0359077P.	DE	Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C345.
PR	29-MAR-2002; 2002US-0368809P.	XX	
PR	04-APR-2002; 2002US-0370110P.	XX	
PR	12-APR-2002; 2002US-0372246P.	KW	Human; differential expression; cancer; angiogenic disorder;
PR	05-JUN-2002; 2002US-0386614P.	KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
PR	16-JUL-2002; 2002US-0396839P.	KW	inflammatory disease; autoimmune disease;
PR	22-JUL-2002; 2002US-0397775P.	KW	retinal neovascularisation syndrome; scarring; uterine fibroid;
PR	22-JUL-2002; 2002US-0397775P.	KW	detection; diagnosis; prognosis; drug screening; drug targeting;
PR	09-SEP-2002; 2002US-0409450P.	KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;
XX		KW	vulnery; gene therapy; vaccine.
PA	(EOSB-) EOS BIOTECHNOLOGY INC.	OS	
XX		OS	Homo sapiens.
PI	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;	PN	
PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;	PN	WO2003042661-A2.
XX		XX	
DR	WPI: 2003-468649/44.	PD	22-MAY-2003.
DR	N-PSDB; ADN39103.	XX	
XX		PF	13-NOV-2002; 2002WO-US036810.
PT	Determining the presence or absence of a pathological cell in a patient,	XX	
PT	useful for diagnosing, prognosing or treating cancer, comprises detecting	PR	13-NOV-2001; 2001US-0350666P.
PT	a nucleic acid in a biological sample.	PR	21-NOV-2001; 2001US-0332464P.
XX		PR	29-NOV-2001; 2001US-0334393P.
PS	Claim 12; SEQ ID NO 422; 1385pp; English.	PR	03-DEC-2001; 2001US-0335394P.
XX		PR	14-DEC-2001; 2001US-0340376P.
CC	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)	PR	08-JAN-2002; 2002US-0347211P.
CC	whose expression is upregulated or downregulated in specific cancers or	PR	10-JAN-2002; 2002US-0347349P.
CC	other diseases such as angiogenic or fibrotic disorders, and to methods	PR	08-FEB-2002; 2002US-0355250P.
CC	of determining the presence or absence of a pathological cell in a	PR	13-FEB-2002; 2002US-0356714P.
CC	patient by detecting a nucleic acid at least 80% identical to those of	PR	20-FEB-2002; 2002US-0359077P.
CC	the invention or by detecting a polypeptide of the invention. The	PR	29-MAR-2002; 2002US-0368809P.
CC	invention also relates to expression vectors and host cells comprising a	PR	04-APR-2002; 2002US-0370110P.
CC	nucleic acid of the invention; antibodies which specifically bind a	PR	12-APR-2002; 2002US-0372246P.
CC	polypeptide of the invention; use of such antibodies for drug targeting;	PR	05-JUN-2002; 2002US-0386614P.
CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,	PR	16-JUL-2002; 2002US-0396839P.
CC	antibodies and methods are useful for diagnosing, prognosing and treating	PR	22-JUL-2002; 2002US-0397775P.
CC	cancer and other conditions such as psoriasis, ischaemia, heart disease,	PR	22-JUL-2002; 2002US-0397775P.
CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal	PR	09-SEP-2002; 2002US-0409450P.
CC	neovascularisation syndromes, scarring and uterine fibroids. They may	XX	
CC	also be useful in wound healing and in contraception. The present	XX	
CC	sequence represents a polypeptide of the invention.	XX	
XX		XX	
SQ	Sequence 223 AA;	XX	
Query Match 83.9%; Score 187; DB 7; Length 223;			
Best Local Similarity 100.0%; Pred. No. 1.3e-162;			
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	37 EVTKVATQKRSQPLNWTSHFGVETGSAAGWGPEEPLPYSRAPFGEGASARPCRCNGGT 96	XX	
DB	37 EVTKVATQKRSQPLNWTSHFGVETGSAAGWGPEEPLPYSRAPFGEGASARPCRCNGGT 96	XX	
QY	97 CVLGSFVCVCPAHTFGYCEHDQRRSECCALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156	XX	
DB	97 CVLGSFVCVCPAHTFGYCEHDQRRSECCALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156	XX	
QY	157 CDPKDFLASHAHGSPAGASLSLLLLPCALLHRLLRDPDAHPRLSVLPVQRRPCGR 216	XX	
DB	157 CDPKDFLASHAHGSPAGASLSLLLLPCALLHRLLRDPDAHPRLSVLPVQRRPCGR 216	XX	
QY	217 PGLGHRL 223	XX	
DB	217 PGLGHRL 223	XX	

CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.  
XX  
SQ Sequence 223 AA;  
Query Match 83.9%; Score 187; DB 7; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 37 EVTKVATQKIQRSPLNWTSSHFGEVTSAGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96  
DB 37 EVTKVATQKIQRSPLNWTSSHFGEVTSAGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96  
QY 97 CVLGSCVCPAHTFTGRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 97 CVLGSCVCPAHTFTGRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
QY 157 CDPKDFLASHAHGSPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216  
DB 157 CDPKDFLASHAHGSPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216  
QY 217 PGLGHRLL 223  
DB 217 PGLGHRLL 223  
RESULT 12  
ADY85963  
ID ADY85963 standard; protein; 223 AA.  
XX  
AC ADY85963;  
DT 16-JUN-2005 (first entry)  
XX Human CRIPTIC protein, a member of the EGF-CFC family Seq 4.  
XX cell signaling; oncogenesis; antisense therapy; cytostatic; mutagenesis;  
KW protein interaction; oncoprotein.  
XX  
XX Homo sapiens.  
XX WO2005028433-A2.  
XX  
XX 31-MAR-2005.  
XX  
XX 14-SEP-2004; 2004WO-US029967.  
XX  
XX 15-SEP-2003; 2003US-0503046P.  
XX (RERE-) RES DEV FOUND.  
XX  
XX Vale W, Gray PC, Harrison CA;  
XX WPI; 2005-242562/25.  
XX  
XX Augmenting signaling of a ligand of receptor serine kinase in a cell  
PT comprises inhibiting the formation of complexes between Crip1 and the  
PT ligand on the surface of the cell.  
XX  
XX Disclosure; SEQ ID NO 4; 60pp; English.  
XX  
XX This invention relates to a novel method for augmenting signaling of a  
CC ligand of a receptor serine kinase within a cell by inhibiting the  
CC formation of complexes between Crip1 and this ligand on the surface of  
CC the cell. Specifically, it refers to TGF-beta and activin which are the  
CC ligands of serine kinase receptors and which regulate tissue homeostasis  
CC by activating the Smad2/3 intracellular signaling pathway; disruption of  
CC this signaling pathway is associated with oncogenesis and tumorigenesis.  
CC As such, the present invention describes a method for augmenting Smad2/3  
CC signaling in a cell by administering a mutant ligand that retains  
CC signaling activity but is unable to bind to Crip1, and thus bypasses  
CC antagonism by Crip1. Note that augmentation of signaling increases  
CC phosphorylation and activation of Smad2 and Smad3 in the cell, such that

CC it decreases the proliferative rate of the cell. The receptor serine  
CC kinase is a type I activin receptor-like kinase-4 or -5 (ALK-4 or ALK-5)  
CC and the formation of complexes is inhibited by suppressing expression of  
CC Crip1 using antisense oligonucleotides (siRNA) directed against Crip1,  
CC and also mutating at least one allele of Crip1 by homologous  
CC recombination. Accordingly, pharmaceutical compositions derived thereof  
CC exhibit cytostatic activity. This polypeptide sequence is the human  
CC Crip1 protein, a member of the EGF-CFC (Epidermal Growth Factor-Crip1,  
CC FRL-1, Crip1) family of proteins of the invention.  
XX  
SQ Sequence 223 AA;  
Query Match 83.9%; Score 187; DB 9; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 37 EVTKVATQKIQRSPLNWTSSHFGEVTSAGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96  
DB 37 EVTKVATQKIQRSPLNWTSSHFGEVTSAGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96  
QY 97 CVLGSCVCPAHTFTGRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 97 CVLGSCVCPAHTFTGRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
QY 157 CDPKDFLASHAHGSPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216  
DB 157 CDPKDFLASHAHGSPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216  
QY 217 PGLGHRLL 223  
DB 217 PGLGHRLL 223  
RESULT 13  
AAU16957  
ID AAU16957 standard; protein; 231 AA.  
XX  
AC AAU16957;  
DT 07-NOV-2001 (first entry)  
XX  
XX Human novel secreted protein, SEQ ID 198.  
XX  
XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;  
KW cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective;  
KW antibacterial; virucide; fungicide; opthalmological; vulnary;  
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;  
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
KW cerebral ischaemia; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; epithelial cell proliferation; skin ageing; food additive;  
KW preservative; antiproliferative.  
XX  
XX Homo sapiens.  
XX  
XX WO200155441-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001320.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 24-FEB-2000; 2000US-0184664P.  
XX 02-MAR-2000; 2000US-0186350P.  
XX 16-MAR-2000; 2000US-0189874P.  
XX 17-MAR-2000; 2000US-0190076P.  
XX 18-MAR-2000; 2000US-0198123P.  
XX 19-APR-2000; 2000US-0205515P.  
XX 07-JUN-2000; 2000US-0209467P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 30-JUN-2000; 2000US-0215135P.  
XX 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 03-SEP-2000; 2000US-0229509P.  
PR 03-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
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PR 14-SEP-2000; 2000US-0233063P.  
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PR 21-SEP-2000; 2000US-0234223P.  
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PR 23-SEP-2000; 2000US-0234997P.  
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PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
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PR 20-OCT-2000; 2000US-0241808P.

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PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476222/51.

N-PSDB; AAS26862.

Novel polypeptides and polynucleotides useful as diagnostic reagents to  
diagnose diseases or disorders associated with aberrant expression or  
activity of polypeptides, for treating blood clotting disorder,  
hemophilia.

Claim 11; SEQ ID NO 198; 601pp; English.

The invention relates to isolated nucleic acid molecules and their  
encoded secreted proteins. The nucleic acids and proteins are used to  
prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
in diagnosing a pathological condition or susceptibility to a  
pathological condition. Antibodies to the proteins can also be used in  
alleviating symptoms associated with the disorders and in diagnostic

CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays  
CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
CC and many other disorders listed in the specification. The polypeptides  
CC can also be used to aid wound healing and epithelial cell proliferation,  
CC to prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence represents a novel secreted protein of the invention. Note: The

Query Match 83.9%; Score 187; DB 4; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1.3e-162;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 37 EVTKVATQKHRSQPLNWTSSHFGEVGTSAEGWGPEEPPLYSRAFGGASARPRCCRNNGT 96  
DB 45 EVTKVATQKHRSQPLNWTSSHFGEVGTSAEGWGPEEPPLYSRAFGGASARPRCCRNNGT 104  
QY 97 CVLGSFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 105 CVLGSFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164  
QY 157 CDPKDFLASHAHGSPSAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216  
DB 165 CDPKDFLASHAHGSPSAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 224  
QY 217 PGLGHRLL 223  
DB 225 PGLGHRLL 231

RESULT 14  
AAW09111  
ID AAW09111 standard; protein; 230 AA.

AC AAW09111;  
XX  
XX 16-APR-1997 (first entry)  
DT Human criptin growth factor.  
DE  
XX  
XX Criptin growth factor; CGF; angiogenesis; wound healing; vulnerary;  
KW muscle wastage; osteoporosis; implant fixation; tissue regeneration;  
KW pancreas cancer; diagnosis; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= sig\_peptide  
XX  
XX WO9639420-A1.  
XX  
PD 12-DEC-1996.  
XX  
XX 05-JUN-1995; 95WO-US007087.  
XX  
XX 05-JUN-1995; 95WO-US007087.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Meisner PS, Coleman TA;  
XX  
XX WPI; 1997-043055/04.  
XX  
XX N-PSDB; AAT51058.

PT New isolated human Criptin Growth Factor polypeptide - which can be used  
PT to stimulate angiogenesis and develop products for use in diagnosis and  
PT therapy.

XX  
PS Claim 12; Fig 1; 52pp; English.

XX Human criptin growth factor (CGF) (AAW09111) is a novel polypeptide  
CC structurally related to human cripto growth factor. It is overexpressed  
CC and secreted by certain types of cancer cells, e.g. pancreatic cancers.  
CC Recombinant CGF can be produced in host cells utilising vectors  
CC incorporating a CGF cDNA clone (AAT51058) isolated from a human  
CC pancreatic cancer tissue cDNA library. CGF can be used to treat e.g.  
CC muscle wasting diseases, osteoporosis, to aid implant fixation, to  
CC stimulate tissue regeneration and wound healing, to promote angiogenesis  
CC and to stimulate proliferation of vascular smooth muscle and endothelial  
CC cell prodn. It can also be used as a marker for cancer diagnosis

SQ Sequence 230 AA;

Query Match 66.8%; Score 149; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 8.1e-128;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 EVTKVATQKHRSQPLNWTSSHFGEVGTSAEGWGPEEPPLYSRAFGGASARPRCCRNNGT 96  
DB 37 EVTKVATQKHRSQPLNWTSSHFGEVGTSAEGWGPEEPPLYSRAFGGASARPRCCRNNGT 96  
QY 97 CVLGSFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 97 CVLGSFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
QY 157 CDPKDFLASHAHGSPSAGGAPSLLLLPCCA 185  
DB 157 CDPKDFLASHAHGSPSAGGAPSLLLLPCCA 185

RESULT 15  
AAG77914  
ID AAG77914 standard; protein; 223 AA.

XX AAG77914;  
XX  
XX 23-JAN-2002 (first entry)  
DT Human cryptic-like polypeptide.  
DE  
XX  
XX Cryptic; human; cytostatic; cardiant; nootropic; neuroleptic; cancer;  
KW antiasthmatic; anti-angiogenic; gene therapy; lung cancer; asthma;  
KW respiratory disease; epilepsy; schizophrenia; depression; hyperactivity;  
KW heart hypertrophy; heart failure; cardiomyopathy; angiogenesis;  
KW vasculogenesis.  
XX  
XX Homo sapiens.  
XX  
XX WO200177322-A1.  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-EP003965.  
XX  
XX 10-APR-2000; 2000EP-00107142.  
XX  
XX (MERE ) MERCK PATENT GMBH.  
XX  
XX Duecker K;  
XX  
XX WPI; 2002-017462/02.  
XX  
XX N-PSDB; AAH77168.  
XX  
XX Novel cryptic-like secreted polypeptide found in various tumors and  
PT organs is useful to treat diseases including cancer, particularly lung  
PT cancer, asthma and heart disease.  
PT

PS Claim 1; Page 33-34; 37pp; English.

XX The sequence represents the novel human cryptic-like secreted protein of  
CC the invention. The polypeptide of the invention has cytostatic, cardiant,  
CC neurotropic, neuroleptic, antiasthmatic, and anti-angiogenic activity, and  
CC has a use in gene therapy. The polypeptide and polynucleotide of the  
CC invention may be used to treat cancer, particularly lung cancer,  
CC respiratory diseases, asthma, epilepsy, schizophrenia, depression,  
CC hyperactivity, heart hypertrophy, heart failure, cardiomyopathies,  
CC aberrant angiogenesis and vasculogenesis

Sequence 223 AA;

Query Match	65.0%;	Score 145;	DB 5;	Length 223;
Best Local Similarity	100.0%;	Prod. No. 3.6e-124;		
Matches 145;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	79	AFEGASAPRCCRNNGTCVLGSCVCPAHTTGRYCEHDORRSCGALEHGAWTLRACHL	138	
Qy	139	CRCIFGALHCLPLQTPDRCDPKPLASHANGPSAGGAPSLLLLLPCALLHRLLRDPAPAH	198	
Db	139	CRCIFGALHCLPLQTPDRCDPKPLASHANGPSAGGAPSLLLLLPCALLHRLLRDPAPAH	198	
Qy	199	PSLVPVQLORRRPCRGPLGHRL	223	
Db	199	PSLVPVQLORRRPCRGPLGHRL	223	

Search completed: September 7, 2006, 12:18:51  
Job time : 192 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 11:44:20 ; Search time 196 Seconds  
(without alignments)  
520.200 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 1249

Sequence: 1 MTRHHVRLFTVSLALQII.....PSVLQRERRPCRGRLGHLRL 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*
- 10: Geneseq2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1249	100.0	223	8	ADO05060 Human cri
2	1249	100.0	229	4	AAU18122 Novel hum
3	1249	100.0	229	4	AAU17028 Human nov
4	1249	100.0	229	4	ABU10300 Human cdn
5	1249	100.0	229	4	AAU19904 Novel hum
6	1249	100.0	229	5	ABJ05749 Novel hum
7	1249	100.0	229	5	ABP68887 Human pol
8	1242	99.4	231	4	AAU16957 Human nov
9	1241	99.4	223	5	ABB90336 Human pol
10	1241	99.4	223	6	ABU56711 Lung canc
11	1241	99.4	223	7	ADN39104 Cancer/an
12	1241	99.4	223	7	ADN39975 Cancer/an
13	1241	99.4	223	9	ADY85963 Human cri
14	1233	98.7	223	5	AAG77914 Human cry
15	1044	83.6	230	2	AAW09111 Human cri
16	488	39.1	202	9	ADY85962 Murine Cr
17	275.5	22.1	190	9	ADY85965 Zebrafish
18	267	21.4	171	8	ADY88690 Amino aci
19	267	21.4	171	9	ADZ42246 Mouse Cri
20	264	21.1	156	8	ADS88691 Amino aci
21	264	21.1	166	8	ADS88692 Amino aci
22	256	20.5	171	9	ADY85960 Murine Cr
23	255.5	20.5	129	8	ADS88693 Amino aci

24	255.5	20.5	139	8	ADS88694 Sequence
25	249.5	20.0	190	9	ADY85964 African c
26	248.5	19.9	190	2	AAR90768 FGF recep
27	238	19.1	360	5	ABB77107 Human Cri
28	238	19.1	367	5	ABB77106 Human Cri
29	237.5	19.0	188	2	AAW29735 Homo sapi
30	233.5	18.7	188	8	ADS88697 Amino aci
31	233	18.7	129	5	ABB77104 Human Cri
32	233	18.7	139	5	ABB77103 Human Cri
33	233	18.7	173	8	ADS88698 Amino aci
34	233	18.7	174	2	AAR13326 Recombina
35	233	18.7	174	2	AAW32107 Recombina
36	233	18.7	174	8	ADO05065 Human cri
37	233	18.7	183	8	ADS88699 Amino aci
38	233	18.7	188	2	AAR22548 Human CRI
39	233	18.7	188	2	AAW87630 Human CRI
40	233	18.7	188	5	ABB77101 Human Cri
41	233	18.7	188	5	AAO14638 Human cri
42	233	18.7	188	5	AAO14636 Human cri
43	233	18.7	188	5	AAO14727 Human var
44	233	18.7	188	6	ABP97176 Tumour-as
45	233	18.7	188	6	ABP58131 Human Cri

## ALIGNMENTS

RESULT 1  
ADO05060  
ID ADO05060 standard; protein; 223 AA.  
XX  
AC ADO05060;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human criptin growth factor (CGF) protein.

Criptin growth factor; CGF; wound healing; tissue regeneration;  
implant fixation; angiogenesis; neoplasia; tumour; gene therapy; human.  
XX Homo sapiens.  
XX US2004086967-A1.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-SEP-2003; 2003US-00665602.  
XX  
PR 06-JUN-1995; 95US-00471371.  
PR 09-SEP-1999; 99US-00393023.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA Meissner PS, Coleman TA;  
XX  
DR WPI: 2004-356201/33.  
DR N-PSDB; ADO05059.  
XX  
PT New human polynucleotides encoding human criptin growth factor  
PT polypeptides, useful for wound healing or tissue regeneration,  
PT stimulating implant fixation and angiogenesis, and for treating and/or  
PT preventing tumor.

PS Claim 12; SEQ ID NO 2; 19pp; English.

XX The invention provides criptin growth factor (CGF) polypeptides and their  
XX encoding polynucleotides. The invention is useful for wound healing and  
XX tissue regeneration, stimulating implant fixation, angiogenesis and for  
XX treating and preventing neoplasia such as tumour. The invention is also  
XX useful in gene therapy. The present sequence is human criptin growth  
XX factor (CGF) protein.  
SQ Sequence 223 AA;

Query Match		100.0%;	Score 1249;	DB 8;	Length 223;
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Qy	1	MTWRHHVRLLTYSALQIINLGNSYQREKHNGRGVTKVATQKHQSPLNWTS	SHFGE 60		
Db	1	MTWRHHVRLLTYSALQIINLGNSYQREKHNGRGVTKVATQKHQSPLNWTS	SHFGE 60		
Qy	61	VTGSAECGWGPEEPLPYSGAFEGASAPRCRCRNGGTCVLGSCFVCVPAHFTGRYCEHDQRR	120		
Db	61	VTGSAECGWGPEEPLPYSGAFEGASAPRCRCRNGGTCVLGSCFVCVPAHFTGRYCEHDQRR	120		
Qy	121	SECGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGAPSLLL	180		
Db	121	SECGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGAPSLLL	180		
Qy	181	LLPCALLHRLRPDAPAHPRSLVPSVLQRRRCRPGRLGHLR	223		
Db	181	LLPCALLHRLRPDAPAHPRSLVPSVLQRRRCRPGRLGHLR	223		
RESULT 2					
AAU18122					
ID	AAU18122 standard; protein; 229 AA.				
XX	AAU18122;				
AC					
XX					
DT	21-NOV-2001 (first entry)				
XX					
DE	Novel human uterine motility-association polypeptide #29.				
XX					
KW	Human; uterine motility-association disorder; uterus; pregnancy; labour;				
KW	menstrual cycle; gene therapy.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200155201-A1.				
XX					
PD	02-AUG-2001.				
XX					
PF	17-JAN-2001; 2001WO-US0001317.				
XX					
PR	31-JAN-2000;	2000US-0179065P.			
PR	04-FEB-2000;	2000US-0180628P.			
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PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI  
XX  
XX WPI; 2001-488777/53.  
DR N-PSDB; AAS28964.  
XX  
XX New nucleic acid molecules encoding 49 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives.  
XX  
XX Claim 11; SEQ ID NO 98; 524pp; English.  
PS  
XX The present invention relates to the isolation of novel human uterine  
CC motility-association polypeptides, and cDNA (AAS28936-AAS28994) and  
CC genomic sequences encoding for these polypeptides. The sequences of the  
CC invention are useful in the diagnosis, treatment, prevention and/or  
CC prognosis of diseases associated with uterine motility such as pregnancy  
CC and labour, and menstrual disorders. The polynucleotide sequences of the  
CC invention are also useful in gene therapy. AAU18094-AAU18152 represent  
CC novel human uterine motility-association polypeptides. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 229 AA;  
Query Match 100.0%; Score 1249; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 2.1e-95;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 67 VTGSAEGMGPEEPLPYSAFGEASAPRCCRNNGTCTVLGSCFVCVCPAHTGTRYCEHQR 126

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Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 186  
Qy 181 LLPCALLHRLRLDPADAPRSLVPSVLORRRPCGRPLGHRL 223  
Db 187 LLPCALLHRLRLDPADAPRSLVPSVLORRRPCGRPLGHRL 229

RESULT 3  
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XX  
AC AAU17028;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human novel secreted protein, SEQ ID 269.  
XX  
KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;  
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;  
KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;  
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;  
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
KW cerebral ischaemia; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; epithelial cell proliferation; skin ageing; food additive;  
KW preservative; antiproliferative.  
XX  
OS Homo sapiens.  
XX  
PN WO200155441-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001320.  
XX  
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 XX  
 (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-476222/51.  
 DR N-PSDB; AAS26933.  
 XX  
 PT Novel polypeptides and polynucleotides useful as diagnostic reagents to  
 PT diagnose diseases or disorders associated with aberrant expression or  
 PT activity of polypeptides, for treating blood clotting disorder,  
 PT hemophilia.  
 XX  
 PS Claim 11; SEQ ID NO 269; 601pp; English.  
 CC The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Antibodies to the proteins can also be used in  
 CC alleviating symptoms associated with the disorders and in diagnostic  
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays  
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
 CC and many other disorders listed in the specification. The polypeptides  
 CC can also be used to aid wound healing and epithelial cell proliferation,  
 CC to prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence represents a novel secreted protein of the invention. Note: The

Query Match 100.0%; Score 1249; DB 4; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-95;  
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 7 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGCEVTKVATQKHQSPLNWTSHFGE 66  
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PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
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PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-465568/50.  
XX N-PSDB; AAS31589.  
DR Isolated nucleic acid molecule encoding a calcium-binding protein is used  
DR in preventing, treating or ameliorating a medical condition.  
XX Claim 11; SEQ ID NO 101; 542pp; English.  
XX The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19892-AAU19969 represent the novel human calcium-binding proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 229 AA;  
SQ  
Query Match 100.0%; Score 1249; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 2.1e-95;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTWRHVRLLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKHRSPLNWTSSHFGE 60  
Db 7 MTWRHVRLLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKHRSPLNWTSSHFGE 66  
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ID ABJ05749 standard; protein; 229 AA.  
XX ABJ05749;  
XX 14-NOV-2002 (first entry)  
XX



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 KW antiparkinsonian; antitickling; antianemic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antiallergic; antidiabetic; antulcer; anticonvulsant; antifungal;  
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002090672-A1.  
 PN  
 XX 11-JUL-2002.  
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 XX 17-JAN-2001; 2001US-00764853.  
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 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 22-AUG-2000; 2000US-0226868P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234977P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0237040P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 XX  
 XX Rosen CA, Ruben SM, Barash SC;  
 PI

XX WPI; 2002-681727/73.  
 DR N-PSDB; ABV83859.  
 XX  
 PT Novel polypeptide useful for diagnosis, prognosis, prevention, and  
 PT treatment of immune, hyperproliferative, renal, respiratory,  
 PT cardiovascular, reproductive, endocrine, gastrointestinal and  
 PT neurological disorders.  
 XX  
 PS Claim 11; SEQ ID NO 608; 369pp + Sequence Listing; English.  
 XX  
 CC The invention relates to novel genes (ABV83682-ABV84101) and proteins  
 CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 229 AA;  
 Query Match 100.0%; Score 1249; DB 5; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-95;  
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 60  
 DB 7 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGEVTKVATQKIQRSPLNWTSSHFGE 66  
 QY 61 VTGSAEGMGPEEPLPYSRAPGEGASARPRCCRNNGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
 DB 67 VTGSAEGMGPEEPLPYSRAPGEGASARPRCCRNNGTCVLGSCFVCPAHFTGRYCEHDQRR 126  
 QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180  
 DB 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186  
 QY 181 LLPCALLHRLRPDAPAHPSLVPSVLQRRRRCGRPGGLGHLR 223  
 DB 187 LLPCALLHRLRPDAPAHPSLVPSVLQRRRRCGRPGGLGHLR 229  
 RESULT 8  
 AAU16957  
 ID AAU16957 standard; protein; 231 AA.  
 XX  
 AC AAU16957;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Human novel secreted protein, SEQ ID 198.  
 XX  
 KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;  
 KW cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotective;  
 KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;  
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;  
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
 KW cerebral ischaemia; angiogenesis; nervous system disorder;  
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;  
 KW preservative; antiproliferative.  
 XX  
 OS Homo sapiens.

PR PR PR PR



PI Rosen CA, Barash SC, Ruben SM;  
XX WPI: 2001-476222/51.  
DR N-PSDB; AAS26862.  
XX  
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to  
PT diagnose diseases or disorders associated with aberrant expression or  
PT activity of polypeptides, for treating blood clotting disorder,  
PT hemophilia.  
XX  
XX Claim 11; SEQ ID NO 198; 601pp; English.  
PS  
XX The invention relates to isolated nucleic acid molecules and their  
XX encoded secreted proteins. The nucleic acids and proteins are used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
CC in diagnosing a pathological condition or susceptibility to a  
CC pathological condition. Antibodies to the proteins can also be used in  
CC alleviating symptoms associated with the disorders and in diagnostic  
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays  
CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodenesis,  
CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
CC and many other disorders listed in the specification. The polypeptides  
CC can also be used to aid wound healing and epithelial cell proliferation,  
CC to prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence represents a novel secreted protein of the invention. Note: The  
Query Match 99.4%; Score 1242; DB 4; Length 231;  
Best Local Similarity 99.6%; Pred. No. 8e-95;  
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGRGVEVTKVATQKHQKQSLNWTSSHFGE 60  
Db 9 MTRHHVRLFTVSLALQIINLGNVQREKHNGRGVEVTKVATQKHQKQSLNWTSSHFGE 68  
QY 61 VTGSAGWGPEEPLPYSRAPFEGASARPCRCRNGGTCVLGSCFVCPAHFTGRCEHDQRR 120  
Db 69 VTGSAGWGPEEPLPYSRAPFEGASARPCRCRNGGTCVLGSCFVCPAHFTGRCEHDQRR 128  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSLLL 180  
Db 129 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSLLL 188  
QY 181 LLPCALLHRLLRDPADPAHPRSLVPSVLQRRRRCGRPGLGHRL 223  
Db 189 LLPCALLHRLLRDPADPAHPRSLVPSVLQRRRRCGRPGLGHRL 231  
RESULT 9  
ABB90336  
ID ABB90336 standard; protein; 223 AA.  
XX  
AC ABB90336;  
XX  
DT 24-MAY-2002 (first entry)  
XX  
XX Human polypeptide SEQ ID NO 2712.  
XX  
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
KW vulnerary; anticoagulant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.  
XX

OS Homo sapiens.  
XX WO200190304-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 18-MAY-2001; 2001WO-US016450.  
XX  
XX 19-MAY-2000; 2000US-0205515P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Birse CE, Rosen CA;  
XX WPI: 2002-122018/16.  
DR N-PSDB; ABL90745.  
XX  
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
PT prevention of neural, immune system, muscular, reproductive,  
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
PT disorders.  
XX  
XX Claim 11; SEQ ID NO 2712; 2081pp + Sequence Listing; English.  
PS  
XX The invention relates to novel genes (ABL9449-ABL90853) and proteins  
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemia; and (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at fcp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 223 AA;  
Query Match 99.4%; Score 1241; DB 5; Length 223;  
Best Local Similarity 99.6%; Pred. No. 9.3e-95;  
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGRGVEVTKVATQKHQKQSLNWTSSHFGE 60  
Db 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGRGVEVTKVATQKHQKQSLNWTSSHFGE 60  
QY 61 VTGSAGWGPEEPLPYSRAPFEGASARPCRCRNGGTCVLGSCFVCPAHFTGRCEHDQRR 120  
Db 61 VTGSAGWGPEEPLPYSRAPFEGASARPCRCRNGGTCVLGSCFVCPAHFTGRCEHDQRR 120  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSLLL 180  
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSLLL 180  
QY 181 LLPCALLHRLLRDPADPAHPRSLVPSVLQRRRRCGRPGLGHRL 223  
Db 181 LLPCALLHRLLRDPADPAHPRSLVPSVLQRRRRCGRPGLGHRL 223  
RESULT 10  
ABU56711  
ID ABU56711 standard; protein; 223 AA.  
XX  
AC ABU56711;  
XX  
DT 02-APR-2003 (first entry)  
XX

DE Lung cancer-associated polypeptide #304.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;

KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

OS Unidentified.

XX WO200286443-A2.

PN 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012476.

PF 18-APR-2001; 2001US-0284770P.

PR 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

PI WPI; 2003-093161/08.

DR N-PSDB; ABX76440.

XX Detecting a lung cancer-associated transcript in a cell from a patient

PT for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer.

XX Claim 27; Page 426; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated

CC transcript in a cell from a patient, comprising contacting a biological

CC sample from the patient with a polynucleotide that selectively hybridises

CC to a sequence that is at least 80 % identical to a gene that exhibits

CC increased or decreased expression in lung cancer samples. Lung cancer-

CC associated polynucleotides and polypeptides are used for identifying a

CC compound that modulates a lung cancer-associated polypeptide, for

CC inhibiting proliferation of a lung cancer-associated cell to treat lung

CC cancer in a patient and for treating a mammal having lung cancer by

CC administering a modulatory compound identified. The methods are useful

CC for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,

CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful

CC for diagnostic purposes and as targets for screening for therapeutic

CC compounds that modulate lung cancer, such as antibodies. Sequences

CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the

CC invention

XX Sequence 223 AA;

SQ

Query Match 99.4%; Score 1241; DB 6; Length 223;

Best Local Similarity 99.8%; Pred. No. 9.3e-95;

Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGREVTKVATQKHQSPLNWTSFHGE 60

DB 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGREVTKVATQKHQSPLNWTSFHGE 60

OY 61 VTGSAEGWGPEEPLPYSAFEGASAPRCRRNGGTCVLGSCFVCPAFTGRCVHDQRR 120

DB 61 VTGSAEGWGPEEPLPYSAFEGASAPRCRRNGGTCVLGSCFVCPAFTGRCVHDQRR 120

OY 121 SEGGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180

Db 121 SEGGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180

OY 181 LLPCALIHLRLPPDAPAHPRSLVPSVLQRRPCCGRPGIGHRL 223

DB 181 LLPCALIHLRLPPDAPAHPRSLVPSVLQRRPCCGRPGIGHRL 223

RESULT 11

ADN39104

ID ADN39104 standard; protein; 223 AA.

XX

AC ADN39104;

XX

DT 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:422.

DE Human; differential expression; cancer; angiogenic disorder;

XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

KW inflammatory disease; autoimmune disease;

KW retinal neovascularisation syndrome; scarring; uterine fibroid;

KW detection; diagnosis; prognosis; drug screening; drug targeting;

KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;

XX vulneryary; gene therapy; vaccine.

XX Homo sapiens.

OS WO2003042661-A2.

XX

PN 22-MAY-2003.

PD

XX 13-NOV-2002; 2002WO-US036810.

PF 13-NOV-2001; 2001US-0350666P.

PR 21-NOV-2001; 2001US-0332464P.

PR 29-NOV-2001; 2001US-0334393P.

PR 03-DEC-2001; 2001US-0335394P.

PR 14-DEC-2001; 2001US-0340376P.

PR 08-JAN-2002; 2002US-0347211P.

PR 10-JAN-2002; 2002US-0347349P.

PR 08-FEB-2002; 2002US-0355250P.

PR 13-FEB-2002; 2002US-0356714P.

PR 20-FEB-2002; 2002US-0359077P.

PR 29-MAR-2002; 2002US-0368809P.

PR 04-APR-2002; 2002US-0370110P.

PR 12-APR-2002; 2002US-0372246P.

PR 05-JUN-2002; 2002US-0386614P.

PR 16-JUL-2002; 2002US-0396839P.

PR 22-JUL-2002; 2002US-039775P.

PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX WPI; 2003-468649/44.

DR N-PSDB; ADN39103.

XX

PT Determining the presence or absence of a pathological cell in a patient,

PT useful for diagnosing, prognosing or treating cancer, comprises detecting

PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO 422; 1385pp; English.

PS The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

CC whose expression is upregulated or downregulated in specific cancers or

CC other diseases such as angiogenic or fibrotic disorders, and to methods

CC of determining the presence or absence of a pathological cell in a

CC patient by detecting a nucleic acid at least 80% identical to those of

CC the invention or by detecting a polypeptide of the invention. The

CC invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides, and  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.  
XX  
SQ Sequence 223 AA;

Query Match 99.4%; Score 1241; DB 7; Length 223;  
Best Local Similarity 99.6%; Pred. No. 9.3e-95;  
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGREVTKVATQKHRSPLNWTSSHFGE 60  
DB 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGREVTKVATQKHRSPLNWTSSHFGE 60  
  
QY 61 VTGSAEGWGPEEPLPYSRAFEGASARPRCCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
DB 61 VTGSAEGWGPEEPLPYSRAFEGASARPRCCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180  
DB 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180  
  
QY 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223  
DB 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223

RESULT 12  
ADN39975  
ID ADN39975 standard; protein; 223 AA.  
XX  
AC ADN39975;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C345.  
XX  
DE Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
KW detection; diagnosis; prognosis; drug screening; drug targeting;  
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
KW vulnery; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX W02003042661-A2.  
XX  
XX 22-MAY-2003.  
XX  
XX 13-NOV-2002; 2002WO-US036810.  
XX  
XX 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-0332464P.  
PR 23-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-035250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0368809P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.

PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX  
DR N-PSDB; ADN39758.  
DR WPI; 2003-468649/44.  
DR  
XX  
XX  
PT Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX  
PS Claim 12; SEQ ID NO C345; 1385pp; English.

CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.  
XX  
SQ Sequence 223 AA;

Query Match 99.4%; Score 1241; DB 7; Length 223;  
Best Local Similarity 99.6%; Pred. No. 9.3e-95;  
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGREVTKVATQKHRSPLNWTSSHFGE 60  
DB 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGREVTKVATQKHRSPLNWTSSHFGE 60  
  
QY 61 VTGSAEGWGPEEPLPYSRAFEGASARPRCCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
DB 61 VTGSAEGWGPEEPLPYSRAFEGASARPRCCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
  
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180  
DB 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180  
  
QY 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223  
DB 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223

RESULT 13  
ADY85963  
ID ADY85963 standard; protein; 223 AA.  
XX  
AC ADY85963;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human Cripitic protein, a member of the EGF-CFC family Seq 4.  
XX  
KW cell signaling; oncogenesis; antisense therapy; cytostatic; mutagenesis;  
KW protein interaction; oncoprotein.

```
XX OS Homo sapiens.
XX PN WO2005028433-A2.
XX PD 31-MAR-2005.
XX PF 14-SEP-2004; 2004WO-US029967.
XX PR 15-SEP-2003; 2003US-0503046P.
XX PA (RERE-) RES DEV FOUND.
XX PI Vale W, Gray PC, Harrison CA;
XX PD WPI; 2005-242562/25.
XX PT Augmenting signaling of a ligand of receptor serine kinase in a cell
XX PT comprises inhibiting the formation of complexes between Cripto and the
XX PT ligand on the surface of the cell.
XX PS Disclosure; SEQ ID NO 4; 60pp; English.
XX CC This invention relates to a novel method for augmenting signaling of a
XX CC ligand of a receptor serine kinase within a cell by inhibiting the
XX CC formation of complexes between Cripto and this ligand on the surface of
XX CC the cell. Specifically, it refers to TGF-beta and activin which are the
XX CC ligands of serine kinase receptors and which regulate tissue homeostasis
XX CC by activating the Smad2/3 intracellular signaling pathway; disruption of
XX CC this signaling pathway is associated with oncogenesis and tumorigenesis.
XX CC As such, the present invention describes a method for augmenting Smad2/3
XX CC signaling in a cell by administering a mutant ligand that retains
XX CC signaling activity but is unable to bind to Cripto, and thus bypasses
XX CC antagonism by Cripto. Note that augmentation of signaling increases
XX CC phosphorylation and activation of Smad2 and Smad3 in the cell, such that
XX CC it decreases the proliferative rate of the cell. The receptor serine
XX CC kinase is a type I activin receptor-like kinases-4 or -5 (ALK-4 or ALK-5)
XX CC and the formation of complexes is inhibited by suppressing expression of
XX CC Cripto using antisense oligonucleotides (siRNA) directed against Cripto,
XX CC and also mutating at least one allele of Cripto by homologous
XX CC recombination. Accordingly, pharmaceutical compositions derived thereof
XX CC exhibit cytostatic activity. This polypeptide sequence is the human
XX CC Criptic protein, a member of the EGF-CFC (Epidermal Growth Factor-Cripto,
XX CC FRL-1, Criptic) family of proteins of the invention.
XX SQ Sequence 223 AA;
Query Match 99.4%; Score 1241; DB 9; Length 223;
Best Local Similarity 99.6%; Pred. No. 9.3e-95;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTRWHVRLFTVSLALQIINLNSYQREKHNGRGREVTKVATQKHQSPLNWTSHFGE 60
DB 1 MTRWHVRLFTVSLALQIINLNSYQREKHNGRGREVTKVATQKHQSPLNWTSHFGE 60
QY 61 VTGSAGWGPEEPLPYSRAPFGEGASARPCCRNGGTCVLGSCFCVCPAHTGRYCEHDQRR 120
DB 61 VTGSAGWGPEEPLPYSRAPFGEGASARPCCRNGGTCVLGSCFCVCPAHTGRYCEHDQRR 120
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180
DB 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180
DB 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180
QY 181 LLPCALLHRLLRDPADAPAHPRSLVPSVLQRRRRCGRPGLGHRL 223
DB 181 LLPCALLHRLLRDPADAPAHPRSLVPSVLQRRRRCGRPGLGHRL 223
RESULT 14
AAG77914
ID AAG77914 standard; protein; 223 AA.
XX AC AAG77914;
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XX DT 23-JAN-2002 (first entry)
XX XX Human cryptic-like polypeptide.
XX KW Cryptic; human; cytostatic; cardiant; nootropic; neuroleptic; cancer;
XX KW antiasthmatic; anti-angiogenic; gene therapy; lung cancer; asthma; activity;
XX KW respiratory disease; epilepsy; schizophrenia; depression; hyperactivity;
XX KW heart hypertrophy; heart failure; cardiomyopathy; angiogenesis;
XX KW vasculogenesis.
XX OS Homo sapiens.
XX PN WO200177322-A1.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-EP003965.
XX PR 10-APR-2000; 2000EP-00107142.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Duecker K;
XX DR WPI; 2002-017462/02.
XX DR N-PSDB; AAH77168.
XX PT Novel cryptic-like secreted polypeptide found in various tumors and
XX PT organs is useful to treat diseases including cancer, particularly lung
XX PT cancer, asthma and heart disease.
XX PS Claim 1; Page 33-34; 37pp; English.
XX CC The sequence represents the novel human cryptic-like secreted protein of
XX CC the invention. The polypeptide of the invention has cytostatic, cardiant,
XX CC nootropic, neuroleptic, antiasthmatic, and anti-angiogenic activity, and
XX CC has a use in gene therapy. The polypeptide and polynucleotide of the
XX CC invention may be used to treat cancer, particularly lung cancer,
XX CC respiratory diseases, asthma, epilepsy, schizophrenia, depression,
XX CC hyperactivity, heart hypertrophy, heart failure, cardiomyopathies,
XX CC aberrant angiogenesis and vasculogenesis
XX SQ Sequence 223 AA;
Query Match 98.7%; Score 1233; DB 5; Length 223;
Best Local Similarity 99.1%; Pred. No. 4.3e-94;
Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MTRWHVRLFTVSLALQIINLNSYQREKHNGRGREVTKVATQKHQSPLNWTSHFGE 60
DB 1 MTRWHVRLFTVSLALQIINLNSYQREKHNGRGREVTKVATQKHQSPLNWTSHFGE 60
QY 61 VTGSAGWGPEEPLPYSRAPFGEGASARPCCRNGGTCVLGSCFCVCPAHTGRYCEHDQRR 120
DB 61 VTGSAGWGPEEPLPYSRAPFGEGASARPCCRNGGTCVLGSCFCVCPAHTGRYCEHDQRR 120
QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180
DB 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180
QY 181 LLPCALLHRLLRDPADAPAHPRSLVPSVLQRRRRCGRPGLGHRL 223
DB 181 LLPCALLHRLLRDPADAPAHPRSLVPSVLQRRRRCGRPGLGHRL 223
RESULT 15
AAW09111
ID AAW09111 standard; protein; 230 AA.
XX AC AAW09111;
XX DT 16-APR-1997 (first entry)
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XX Human criptin growth factor.  
DE  
XX  
XX Criptin growth factor; CGF; angiogenesis; wound healing; vulnerary;  
KW muscle wastage; osteoporosis; implant fixation; tissue regeneration;  
KW pancreas cancer; diagnosis; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1. .23  
FT /label= Sig\_peptide  
XX  
XX WO9639420-A1.  
XX  
XX 12-DEC-1996.  
PD  
XX  
XX 05-JUN-1995; 95WO-US007087.  
PF  
XX  
XX 05-JUN-1995; 95WO-US007087.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Meissner PS, Coleman TA;  
PI  
XX  
XX WPI; 1997-043055/04.  
DR N-PSDB; AAT51058.  
DR  
XX  
XX New isolated human Criptin Growth Factor polypeptide - which can be used  
PT to stimulate angiogenesis and develop products for use in diagnosis and  
PT therapy.  
PT  
XX  
XX Claim 12; Fig 1; 52pp; English.  
PS  
XX  
XX Human criptin growth factor (CGF) (AAM09111) is a novel polypeptide  
CC structurally related to human cripto growth factor. It is overexpressed  
CC and secreted by certain types of cancer cells, e.g. pancreatic cancers.  
CC Recombinant CGF can be produced in host cells utilising vectors  
CC incorporating a CGF cDNA clone (AAT51058) isolated from a human  
CC pancreatic cancer tissue cDNA library. CGF can be used to treat e.g.  
CC muscle wasting diseases, osteoporosis, to aid implant fixation, to  
CC stimulate tissue regeneration and wound healing, to promote angiogenesis  
CC and to stimulate proliferation of vascular smooth muscle and endothelial  
CC cell prodn. It can also be used as a marker for cancer diagnosis  
XX  
XX Sequence 230 AA;  
Query Match 83.6%; Score 1044; DB 2; Length 230;  
Best Local Similarity 91.4%; Pred. No. 2e-78;  
Matches 191; Conservative 1; Mismatches 5; Indels 12; Gaps 2;  
Qy 1 MTRHHVRLFTVSLALQIINLNGSYOREKHNGRGGEVTKVATQKHQSPINWTSHFGE 60  
Db 1 MTRHHVRLFTVSLALQIINLNGSYOREKHNGRGGEVTKVATQKHQSPINWTSHFGE 60  
Qy 61 VTGSAEGWGPEEPLPYRAFEGEGASAPRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
Db 61 VTGSAEGWGPEEPLPYRAFEGEGASAPRCRNGGTCVLGSCVCPAHFTGRYCEHDQRR 120  
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180  
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGGAPSLLL 180  
Qy 181 LLPCALLHRLRPDAPA-----HPRSLVP 204  
Db 181 LLPCA-----TPAPASCARMRPRTLGP 202

Search completed: September 7, 2006, 11:54:01  
Job time : 198 secs

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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:35:51 ; Search time 174 Seconds  
(without alignments)  
593.660 Million cell updates/sec

Title: US-10-665-602-2  
Perfect score: 223  
Sequence: 1 MTRWHVRLFTVSLALQII.....PSVLQRERRPCGRPGLGHL 223

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 30

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*  
3: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*  
4: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*  
5: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*  
6: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	223	100.0	223	4	US-10-665-602-2
2	223	100.0	229	3	US-09-764-893-98
3	223	100.0	229	3	US-09-764-881-101
4	223	100.0	229	3	US-09-764-853-608
5	223	100.0	229	3	US-09-764-898-269
6	223	100.0	229	3	US-09-764-881-101
7	223	100.0	229	4	US-10-073-865-98
8	223	100.0	229	4	US-10-242-747-101
9	187	83.9	223	4	US-10-295-027-422
10	187	83.9	223	4	US-10-295-027-1293
11	187	83.9	223	4	US-10-264-237-2712
12	187	83.9	223	5	US-10-940-431-4
13	187	83.9	231	3	US-09-764-898-198
14	145	65.0	223	4	US-10-257-113-2

ALIGNMENTS

RESULT 1  
US-10-665-602-2  
; Sequence 2, Application US/10665602  
; Publication No. US20040086967A1  
; GENERAL INFORMATION:  
; APPLICANT: Meissner, Paul S.  
; Coleman, Timothy A.  
; TITLE OF INVENTION: Human Cripitin Growth Factor

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/665,602  
FILING DATE: 22-Sep-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/393,023A  
FILING DATE: 09-SEP-1999  
APPLICATION NUMBER: US 08/471,371  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marks, Michelle S.  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PF200D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-665-602-2

Query Match 100.0%; Score 223; DB 4; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.4e-196; Indels 0; Gaps 0;  
Matches 223; Conservative 0; Mismatches 0

Qy	1	MTWRHVRLFTVSLALQIIINLGNSTYQREKHNGRGEVTKVATQKHRSPLNWTSSHFG 60
Db	1	MTWRHVRLFTVSLALQIIINLGNSTYQREKHNGRGEVTKVATQKHRSPLNWTSSHFG 60
Qy	61	VTGSAGWGPEEPPLYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDORR 120
Db	61	VTGSAGWGPEEPPLYSRAFEGASARPCRCRNGGTCVLGSCVCPAHFTGRYCEHDORR 120
Qy	121	SECGALEHGAWTURACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180
Db	121	SECGALEHGAWTURACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL 180
Qy	181	LLPCALLHRLLRDPAHPRSLVPSVLQRRRRCGRPGLGHL 223
Db	181	LLPCALLHRLLRDPAHPRSLVPSVLQRRRRCGRPGLGHL 223

RESULT 2  
US-09-764-893-98  
; Sequence 98, Application US/09764893  
; Publication No. US20020086330A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PZ09  
; CURRENT APPLICATION NUMBER: US/09/764,893  
; CURRENT FILING DATE: 2001-01-19  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 98

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; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-893-98

Query Match          100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGGEVTKVATQKHQSPLNWTSSTHSGE 60
Db 7 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGGEVTKVATQKHQSPLNWTSSTHSGE 66

Qy 61 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRCNGGTGTCVLGSCFVCPAHTGTRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRCNGGTGTCVLGSCFVCPAHTGTRYCEHDQRR 126

Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 186

Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHRL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHRL 229

RESULT 3
US-09-764-881-101
; Sequence 101, Application US/09764881
; Publication No. US20020086821A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-101

Query Match          100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGGEVTKVATQKHQSPLNWTSSTHSGE 60
Db 7 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGGEVTKVATQKHQSPLNWTSSTHSGE 66

Qy 61 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRCNGGTGTCVLGSCFVCPAHTGTRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRCNGGTGTCVLGSCFVCPAHTGTRYCEHDQRR 126

Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 186
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Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHRL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHRL 229

RESULT 4
US-09-764-853-608
; Sequence 608, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 608
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-608

Query Match          100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGGEVTKVATQKHQSPLNWTSSTHSGE 60
Db 7 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGGEVTKVATQKHQSPLNWTSSTHSGE 66

Qy 61 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRCNGGTGTCVLGSCFVCPAHTGTRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRCNGGTGTCVLGSCFVCPAHTGTRYCEHDQRR 126

Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 186

Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHRL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHRL 229

RESULT 5
US-09-764-898-269
; Sequence 269, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 269
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-898-269

Query Match 100.0%; Score 223; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.5e-196;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGEVTKVATQKHQSPLNWTSSTHSGE 60  
DB 7 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGEVTKVATQKHQSPLNWTSSTHSGE 66

QY 61 VTGSAGWGPEEPLPYSAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
DB 67 VTGSAGWGPEEPLPYSAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126

QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 180  
DB 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 186

QY 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223  
DB 187 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 229

RESULT 6  
US-09-764-881-101  
; Sequence 101, Application US/09764881  
; Publication No. US20030125246A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ07  
; CURRENT APPLICATION NUMBER: US/09/764,881  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 101  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-881-101

Query Match 100.0%; Score 223; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.5e-196;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGEVTKVATQKHQSPLNWTSSTHSGE 60  
DB 7 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGEVTKVATQKHQSPLNWTSSTHSGE 66

QY 61 VTGSAGWGPEEPLPYSAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
DB 67 VTGSAGWGPEEPLPYSAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126

QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 180  
DB 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 186

QY 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223  
DB 187 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 229

RESULT 7  
US-10-073-865-98  
; Sequence 98, Application US/10073865  
; Publication No. US20030044904A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJZ09C1  
; CURRENT APPLICATION NUMBER: US/10/073,865  
; CURRENT FILING DATE: 2002-02-14  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 98  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: misc\_feature  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-073-865-98

Query Match 100.0%; Score 223; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 1.5e-196;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGEVTKVATQKHQSPLNWTSSTHSGE 60  
DB 7 MTRHHVRLFTVSLALQIINLNSYQREKHNGRGEVTKVATQKHQSPLNWTSSTHSGE 66

QY 61 VTGSAGWGPEEPLPYSAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120  
DB 67 VTGSAGWGPEEPLPYSAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126

QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 180  
DB 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 186

QY 181 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 223  
DB 187 LLPCALLHRLRPDAPAHPSRLVPSVLQRRRRCGRPGLGHRL 229

RESULT 8  
US-10-242-747-101  
; Sequence 101, Application US/10242747  
; Publication No. US20040005577A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ07C1  
; CURRENT APPLICATION NUMBER: US/10/242,747  
; CURRENT FILING DATE: 2002-09-13  
; Prior Application Number: 09/764,881  
; Prior Filing Date: 2001-01-17  
; Prior Application Number: 60/179,065  
; Prior Filing Date: 2000-01-31  
; Prior Application Number: 60/180,628  
; Prior Filing Date: 2000-02-04  
; Prior Application Number: 60/214,886  
; Prior Filing Date: 2000-06-28  
; Prior Application Number: 60/217,487  
; Prior Filing Date: 2000-07-11  
; Prior Application Number: 60/225,758  
; Prior Filing Date: 2000-08-14  
; Prior Application Number: 60/220,963  
; Prior Filing Date: 2000-07-26

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; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-747-101

Query Match      100.0%; Score 223; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRHHVRLFTVSLALQIINLGNVQREKHNGRGVEVTKVATQKHQSPLNWTSSTHFG 60
DB 7 MTRHHVRLFTVSLALQIINLGNVQREKHNGRGVEVTKVATQKHQSPLNWTSSTHFG 66
QY 61 VTGSAEGWGPEEPLPYSRAFEGASAPRCRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
DB 67 VTGSAEGWGPEEPLPYSRAFEGASAPRCRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
QY 121 SECGALEHGAWTTRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGAPSL 180
DB 127 SECGALEHGAWTTRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGAPSL 186
QY 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHRL 223
DB 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHRL 229

RESULT 9
US-10-295-027-422
; Sequence 422, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
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; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 422
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-422

Query Match      83.9%; Score 187; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-163;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 EYTKVATQKHROSPLNWTSSHFGEVGTGSAEGWGPEEPLPYSRAFEGASAPRCRCRNGGT 96
DB 37 EYTKVATQKHROSPLNWTSSHFGEVGTGSAEGWGPEEPLPYSRAFEGASAPRCRCRNGGT 96
QY 97 CVLGSCFVCPAHFTGRYCEHDQRRSECGALEHGAWTTRACHLCRCIFGALHCLPLQTPDR 156
DB 97 CVLGSCFVCPAHFTGRYCEHDQRRSECGALEHGAWTTRACHLCRCIFGALHCLPLQTPDR 156
QY 157 CDPKDFLASHAHGPSAGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRRRCGR 216
DB 157 CDPKDFLASHAHGPSAGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRRRCGR 216
QY 217 PGLGHRL 223
DB 217 PGLGHRL 223

RESULT 10
US-10-295-027-1293
; Sequence 1293, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
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PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1293  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-295-027-1293

Query Match 83.9%; Score 187; DB 4; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.8e-163;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96  
DB 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96

QY 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY 157 CDPKDFLASHAHGSPAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216  
DB 157 CDPKDFLASHAHGSPAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216

QY 217 PGLGHRLL 223  
DB 217 PGLGHRLL 223

RESULT 11  
US-10-264-237-2712  
Sequence 2712, Application US/10264237  
Publication No. US20040009491A1  
GENERAL INFORMATION:  
APPLICANT: Biree et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: P131P1  
CURRENT APPLICATION NUMBER: US/10/264,237  
CURRENT FILING DATE: 2002-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/16450  
PRIOR FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: US 60/205,515  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 2876  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 2712  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-264-237-2712

Query Match 83.9%; Score 187; DB 4; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.8e-163;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96

QY 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY 157 CDPKDFLASHAHGSPAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216  
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QY 217 PGLGHRLL 223  
DB 217 PGLGHRLL 223

RESULT 12  
US-10-940-431-4  
Sequence 4, Application US/10940431  
Publication No. US20050208045A1  
GENERAL INFORMATION:  
APPLICANT: Valle, Wylie  
APPLICANT: Harrison, Craig A.  
APPLICANT: Gray, Peter C.  
TITLE OF INVENTION: Cripto Antagonism of Activin and TGF-  
TITLE OF INVENTION: Signaling  
FILE REFERENCE: D6525  
CURRENT APPLICATION NUMBER: US/10/940,431  
CURRENT FILING DATE: 2004-09-14  
PRIOR APPLICATION NUMBER: 60/503,046  
PRIOR FILING DATE: 2003-09-15  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Macintosh OS 10  
SEQ ID NO 4  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: amino acid sequence of human Criptic protein  
US-10-940-431-4

Query Match 83.9%; Score 187; DB 5; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.8e-163;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96  
DB 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLPYSRAFGEGASARPRCCRNNGT 96

QY 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156  
DB 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY 157 CDPKDFLASHAHGSPAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216  
DB 157 CDPKDFLASHAHGSPAGGAPSLLLLPCCALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216

QY 217 PGLGHRLL 223  
DB 217 PGLGHRLL 223

RESULT 13  
US-09-764-898-1398  
Sequence 198, Application US/09764898  
Patent No. US20020090673A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PJ201  
CURRENT APPLICATION NUMBER: US/09/764,898  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 311  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 198  
LENGTH: 231  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE

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; LOCATION: (44)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-198

Query Match      83.9%; Score 187; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.9e-163; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 45 EVTKVATQKHRQSLNWTSSHFGEVTSAGWGMPPEPLPYSRAFGEGASARPRCCRNNGT 104

QY 97 CVLGSCFCVCPAHTTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 105 CVLGSCFCVCPAHTTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164

QY 157 CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHLLRPDAPAHPRSLVPSVLQRRRPPCGR 216
Db 165 CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHLLRPDAPAHPRSLVPSVLQRRRPPCGR 224

QY 217 PGLGHRL 223
Db 225 PGLGHRL 231

RESULT 14
US-10-257-113-2
; Sequence 2, Application US/10257113
; Publication No. US20030207293A1
; GENERAL INFORMATION:
; APPLICANT: DUCKER, KLAUS
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN
; FILE REFERENCE: MERCK-2519
; CURRENT APPLICATION NUMBER: US/10/257,113
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: EP 00107142.2
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-113-2

Query Match      65.0%; Score 145; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-125;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 79 AFEGASARPRCCRNNGTCLVGSFCVCPAHTTGRYCEHDQRRSECGALEHGAWTLRACHL 138

QY 139 CRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLLLLPCALLHLLRPDAPAH 198
Db 139 CRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLLLLPCALLHLLRPDAPAH 198

QY 199 PRSLVPSVLQRRRPPCGRPGLGHRL 223
Db 199 PRSLVPSVLQRRRPPCGRPGLGHRL 223

Search completed: September 7, 2006, 12:39:18
Job time : 175 secs
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 11:59:20 ; Search time 49 Seconds  
(without alignments)  
398.354 Million cell updates/sec

Title: US-10-665-602-2  
Perfect score: 1249  
Sequence: 1 MTRHHVRLFTVSLALQII.....PSVLQRERRPCGRLGHL 223

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pcp.\*  
4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H COMB.pcp.\*  
5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.\*  
6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pcp.\*  
7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1044	83.6	230	1	US-08-471-371-2
2	264	21.1	160	1	US-08-441-629-7
3	264	21.1	160	2	US-08-776-207-7
4	264	21.1	160	2	US-09-507-773-7
5	264	21.1	160	2	US-10-016-447-7
6	264	21.1	160	5	PCT-US95-09172-7
7	248.5	19.9	190	1	US-08-441-629-4
8	248.5	19.9	190	2	US-08-776-207-4
9	248.5	19.9	190	2	US-09-507-773-4
10	248.5	19.9	190	2	US-10-016-447-4
11	248.5	19.9	190	5	PCT-US95-09172-4
12	233	18.7	174	7	US-07-749-001-3
13	233	18.7	188	1	US-08-154-198-3
14	233	18.7	188	1	US-08-463-335-3
15	233	18.7	188	1	US-08-464-023A-3
16	233	18.7	188	1	US-08-471-371-7
17	233	18.7	188	1	US-09-949-016-8959
18	233	18.7	192	2	US-09-949-016-11113
19	233	18.7	192	2	US-07-749-001-5
20	225	18.0	188	1	US-08-154-198-5
21	225	18.0	188	1	US-08-463-335-5
22	225	18.0	188	1	US-08-464-023A-5
23	225	18.0	192	2	US-09-949-016-7062
24	225	18.0	192	2	US-09-949-016-7062
25	224	17.9	187	7	US-08-471-371-2
26	157	12.6	94	1	US-08-208-008C-14

27	127.5	10.2	713	2	US-08-872-855-5	Sequence 5, Appli
28	123	9.8	495	2	US-10-006-011A-4	Sequence 4, Appli
29	123	9.8	705	2	US-10-006-011A-3	Sequence 3, Appli
30	123	9.8	810	1	US-08-820-170A-34	Sequence 34, Appli
31	123	9.8	810	2	US-09-055-699-34	Sequence 34, Appli
32	123	9.8	810	2	US-09-273-565-34	Sequence 34, Appli
33	123	9.8	810	2	US-09-565-538-34	Sequence 34, Appli
34	123	9.8	810	2	US-09-661-468-34	Sequence 34, Appli
35	123	9.8	810	2	US-09-976-165-34	Sequence 34, Appli
36	123	9.8	4391	2	US-10-006-011A-2	Sequence 2, Appli
37	120.5	9.6	720	2	US-08-872-855-4	Sequence 4, Appli
38	120.5	9.6	722	2	US-08-981-392-12	Sequence 12, Appli
39	120.5	9.6	722	2	US-09-908-322-12	Sequence 12, Appli
40	120.5	9.6	722	2	US-09-310-685-14	Sequence 14, Appli
41	116.5	9.3	2321	2	US-09-230-652-2	Sequence 2, Appli
42	116.5	9.3	2321	2	US-09-612-226B-2	Sequence 2, Appli
43	115.5	9.2	1068	1	US-08-537-210A-2	Sequence 2, Appli
44	115.5	9.2	1068	2	US-09-113-825-2	Sequence 2, Appli
45	115.5	9.2	2556	1	US-08-185-432-17	Sequence 17, Appli

## ALIGNMENTS

RESULT 1  
US-08-471-371-2  
; Sequence 2, Application US/08471371  
; Patent No. 5981215  
; GENERAL INFORMATION:  
; APPLICANT: Meissner, Paul S.  
; APPLICANT: Coleman, Timothy A.  
; TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STEWART & OLSTEIN  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: N.J.  
; COUNTRY: U.S.A.  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,371  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferraro, Gregory D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 32580-455  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 994-1700  
; TELEFAX: (201) 994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 230 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-371-2

Query Match 83.6%; Score 1044; DB 1; Length 230;  
Best Local Similarity 91.4%; Pred. No. 2.6e-100;  
Matches 191; Conservative 1; Mismatches 5; Indels 12; Gaps 2;  
QY 1 MTRHHVRLFTVSLALQIIINLGNVQREKHNGRGVEVTKVATQKROSLNWTSSHFGE 60  
Db 1 MTRHHVRLFTVSLALQIIINLGNVQREKHNGRGVEVTKVATQKROSLNWTSSHFGE 60

QY 61 VTGSAGWGPEEPLPYSRARFEGASARPRCCRRGGTCVLGSCVCPAHTFTGRYCEHDQRR 120  
Db 61 VTGSAGWGPEEPLPYSRARFEGASARPRCCRRGGTCVLGSCVCPAHTFTGRYCEHDQRR 120  
QY 121 SEGGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180  
Db 121 SEGGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180  
QY 181 LLPCALLHRLLRDPARA-----HPRSLVP 204  
Db 181 LLPCA-----TPAPASCARMPRTLGP 202  
RESULT 2  
US-08-441-629-7  
; Sequence 7, Application US/08441629  
; Patent No. 5766923  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Kinoshita, No. 5766923iyuki  
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,629  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/279,217  
; FILING DATE: 22-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: HU95-01A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 160 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-441-629-7

Query Match 21.1%; Score 264; DB 1; Length 160;  
Best Local Similarity 43.5%; Pred. No. 1.7e-19;  
Matches 50; Conservative 7; Mismatches 44; Indels 14; Gaps 2;  
QY 58 FGEVGTG-----SAEGWGPEEPLPYSRAP-----GEGASARPRCCRRGGTCVLGSGFC 103  
Db 20 FGPVAGRDLAIRDNSIWDQKEPAVRDRSFQFVPSVGIQNSKSLNKTCCLLNGGTCILGSGFC 79  
QY 104 VCPAHTFTGRYCEHDQRRSECGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCD 158  
Db 80 ACPPSPFYGRNCEHDVRKEHCGSILHGTWLPKKCSLCRCWHGQJHCLPQTFLPGCD 134

RESULT 3  
US-08-776-207-7  
; Sequence 7, Application US/08776207A

; Patent No. 6080718  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Kinoshita, No. 6080718iyuki  
; TITLE OF INVENTION: Receptor-Ligand Assay  
; FILE REFERENCE: HU95-01A2  
; CURRENT APPLICATION NUMBER: US/08/776,207A  
; CURRENT FILING DATE: 1997-06-23  
; EARLIER APPLICATION NUMBER: PCT/US95/09172  
; EARLIER FILING DATE: 1995-07-19  
; EARLIER APPLICATION NUMBER: 08/441,629  
; EARLIER FILING DATE: 1995-05-15  
; EARLIER APPLICATION NUMBER: 08/279,217  
; EARLIER FILING DATE: 1994-07-22  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-08-776-207-7  
Query Match 21.1%; Score 264; DB 2; Length 160;  
Best Local Similarity 43.5%; Pred. No. 1.7e-19;  
Matches 50; Conservative 7; Mismatches 44; Indels 14; Gaps 2;  
QY 58 FGEVGTG-----SAEGWGPEEPLPYSRAP-----GEGASARPRCCRRGGTCVLGSGFC 103  
Db 20 FGPVAGRDLAIRDNSIWDQKEPAVRDRSFQFVPSVGIQNSKSLNKTCCLLNGGTCILGSGFC 79  
QY 104 VCPAHTFTGRYCEHDQRRSECGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCD 158  
Db 80 ACPPSPFYGRNCEHDVRKEHCGSILHGTWLPKKCSLCRCWHGQJHCLPQTFLPGCD 134

RESULT 4  
US-09-507-773-7  
; Sequence 7, Application US/09507773  
; Patent No. 6399386  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Kinoshita, No. 6399386iyuki  
; TITLE OF INVENTION: Receptor-Ligand Assay  
; FILE REFERENCE: HU95-01A2  
; CURRENT APPLICATION NUMBER: US/09/507,773  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: 08/776,207  
; PRIOR FILING DATE: 1997-06-23  
; PRIOR APPLICATION NUMBER: 08/441,629  
; PRIOR FILING DATE: 1995-05-15  
; PRIOR APPLICATION NUMBER: 08/279,217  
; PRIOR FILING DATE: 1994-07-22  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-507-773-7

Query Match 21.1%; Score 264; DB 2; Length 160;  
Best Local Similarity 43.5%; Pred. No. 1.7e-19;  
Matches 50; Conservative 7; Mismatches 44; Indels 14; Gaps 2;  
QY 58 FGEVGTG-----SAEGWGPEEPLPYSRAP-----GEGASARPRCCRRGGTCVLGSGFC 103  
Db 20 FGPVAGRDLAIRDNSIWDQKEPAVRDRSFQFVPSVGIQNSKSLNKTCCLLNGGTCILGSGFC 79  
QY 104 VCPAHTFTGRYCEHDQRRSECGALEHGAWTIRACHLCRCIFGALHCLPLQTPDRCD 158  
Db 80 ACPPSPFYGRNCEHDVRKEHCGSILHGTWLPKKCSLCRCWHGQJHCLPQTFLPGCD 134

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RESULT 5
US-10-016-447-7
; Sequence 7, Application US/10016447
; Patent No. 6844193
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 6844193iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/10/016,447
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/776,207
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/279,217
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-447-7

Query Match      21.1%; Score 264; DB 2; Length 160;
Best Local Similarity 43.5%; Pred. No. 1.7e-19;
Matches 50; Conservative 7; Mismatches 44; Indels 14; Gaps 2;

QY 58 FGEVTG-----SAEGWGPEEPLPYSRF-----GEGASARPRCCRRGGTCVLGSFC 103
Db 20 FGPVAGRDIAIRDNSIWQKEPAVRDSFQFVPSVGIONSLSLTKCCLNGGTCILGSFC 79
QY 104 VCPAFTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158
Db 80 ACPPSFYGRNCEHDVRKEHCGSILHGTWLPKKSCLRCWHGQLHCLPQTLPGCD 134

RESULT 6
PCT-US95-09172-7
; Sequence 7, Application PC/TUS9509172
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, Noriyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 15-MAY-1995
; APPLICATION NUMBER: PCT/US95/09172
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,217
; FILING DATE: 22-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,629
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-9540
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-441-629-4

Query Match      19.9%; Score 248.5; DB 1; Length 190;
Best Local Similarity 52.9%; Pred. No. 8.4e-18;
Matches 37; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 89 RCRNGGTCVLGSFCVCPAFTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCL 148
```

```
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-09172-7

Query Match      21.1%; Score 264; DB 5; Length 160;
Best Local Similarity 43.5%; Pred. No. 1.7e-19;
Matches 50; Conservative 7; Mismatches 44; Indels 14; Gaps 2;

QY 58 FGEVTG-----SAEGWGPEEPLPYSRF-----GEGASARPRCCRRGGTCVLGSFC 103
Db 20 FGPVAGRDIAIRDNSIWQKEPAVRDSFQFVPSVGIONSLSLTKCCLNGGTCILGSFC 79
QY 104 VCPAFTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158
Db 80 ACPPSFYGRNCEHDVRKEHCGSILHGTWLPKKSCLRCWHGQLHCLPQTLPGCD 134

RESULT 7
US-08-441-629-4
; Sequence 4, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 5766923iyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 15-MAY-1995
; APPLICATION NUMBER: US/08/441,629
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,217
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-441-629-4

Query Match      19.9%; Score 248.5; DB 1; Length 190;
Best Local Similarity 52.9%; Pred. No. 8.4e-18;
Matches 37; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 89 RCRNGGTCVLGSFCVCPAFTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCL 148
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Db	82	KCCQNGGTCTFLGTCICPKQFTGRHCEHRRPASCVGPHGDMTROGCLLCRCVSGVLHC	141
Qy	149	LPLQTFDRCD	158
Db	142	KPESED-CD	150

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RESULT 8
US-08-776-207-4
; Sequence 4, Application US/08776207A
; Patent No. 6080718
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 6080718iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/08/776.207A
; CURRENT FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: PCT/US95/09172
; EARLIER FILING DATE: 1995-07-19
; EARLIER APPLICATION NUMBER: 08/441,629
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/279,217
; EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-08-776-207-4

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Query Match	19.9%	Score 248.5;	DB 2;	Length 190;
Best Local Similarity	52.9%;	Pred. No. 8.4e-18;		
Matches	37; Conservative 13;	Mismatches 19;	Indels 1;	Gaps 1;
Qy	89	RCCRNGETCVLGSFCVCPAHFTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHC	148	
		:::::     :::     :::     :::     :::     :::		
Dd	82	KCCQNGETCFLGTFCICPKQFTGRHCHERRPASCSCGVPHGDWTRQGCLLCRCVSGVLHC	141	
Qy	149	LPLQTDPDRC	158	
		::		
Dd	142	FKPESED-CD	150	

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RESULT 9
US-09-507-773--4
; Sequence 4, Application US/09507773
; Patent No. 639386
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 639386iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/09/507,773
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 08/776,207
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/441,629
; PRIOR FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: 08/279,217
; PRIOR FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-507-773--4

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Query Match 19.9%; Score 248.5; DB 2; Length 190;  
Best Local Similarity 52.9%; Pred. No. 8.4e-18;

[illegible]

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RESULT 10
US-10-016-447-4
; Sequence 4, Application US/10016447
; Patent No. 6844193
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 6844193iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/10/016,447
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/776,207
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/279,217
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-016-447-4

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	Query Match	19.9%	Score 248.5;	DB 2;	Length 190;
	Best Local Similarity	52.9%;	Pred.No. 8.4e-18;		
	Matches 37; Conservative	13;	Mismatches 19;	Indels 1;	Gaps 1;
Qy	89	RCCRNCGTCTVLGSFCVCPAHFTGRYCEHQDORSECGALEHGAWTLRACHLCRCIFGALHC	148		
	:	:::: ::  :: :	:: :: :: :	:  :: :: :	:  :: :: :
Dd	82	KCQQNGGTCTFLGTFCCICPQFTGRGHEHRRPASCSGVPHGDWIROGCLLRCSVGVLHC	141		
Qy	149	LPLQTDPDRCD	158		
	:	: :			
Dd	142	FKPESED-CD	150		

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RESULT 11
PCT-US95-09172-4
; Sequence 4, Application PC/TUS9509172
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, Noriyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US95/09172
; FILING DATE:
; CLASSIFICATION:

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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/279,217  
;; FILING DATE: 22-JUL-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/441,629  
;; FILING DATE: 15-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; REFERENCE/DOCKET NUMBER: HU95-01A PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 190 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
PCT-US95-09172-4  
  
Query Match 19.9%; Score 248.5; DB 5; Length 190;  
Best Local Similarity 52.9%; Pred. No. 8.4e-18;  
Matches 37; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
  
Qy 89 RCRNGSTCVLGSFCVCPAHFTGRCYCHDORRSECCGALHGHAWTLRACHLCRCIFGALHC 148  
Db 82 KCCQNGTCTGLFTFCICPKQFTGRHCEHERRPASCVGPHGDWIRQCLLCRCVGLHC 141  
  
Qy 149 LPLQTPDRCD 158  
Db 142 FKPESED-CD 150  
  
RESULT 12  
5256643-3  
; Patent No. 5256643  
; APPLICANT: Persico, Maria G.; Salomon, David S.  
; TITLE OF INVENTION: HUMAN CRYPTO PROTEIN  
; NUMBER OF SEQUENCES: 18  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/530,165  
; FILING DATE: 29-MAY-1990  
; SEQ ID NO: 3:  
; LENGTH: 174  
5256643-3  
  
Query Match 18.7%; Score 233; DB 7; Length 174;  
Best Local Similarity 39.1%; Pred. No. 3.1e-16;  
Matches 43; Conservative 30; Mismatches 30; Indels 30; Gaps 2;  
  
Qy 68 WGPPEPLPYSRAFEGEGASARPR-----CCRNGSTCVLGSFCVCPAH 108  
Db 38 WPOEEP-----AIRPRSSQVRPPMGIQHSKELNRTCCCLNGTCLMGSCFACPPS 86  
  
Qy 109 FTGRYCEHDORRSECCGALHGHAWTLRACHLCRCIFGALHCLPLQTPDRCD 158  
Db 87 FYGRNCEHDVRKENCSCVPHDWTLPKKCSLCKCMHGLRCFPOAFLPGCD 136  
  
RESULT 13  
US-07-749-001-3  
; Sequence 3, Application US/07749001  
; Patent No. 5264557  
; GENERAL INFORMATION:  
; APPLICANT: Salomon, David S.  
; APPLICANT: Persico, Maria G.  
; TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1615 L Street, N.W.

;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20036  
;; COMPUTER READABLE FORM: disk  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/749,001  
;; FILING DATE: 19910823  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Scott, Watson T.  
;; REGISTRATION NUMBER: 26,581  
;; REFERENCE/DOCKET NUMBER: WTS/5683/91630/SRL  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 861-3000  
;; TELEFAX: (202) 822-0944  
;; TELEX: 248453 CUSH  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 188 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-749-001-3  
  
Query Match 18.7%; Score 233; DB 1; Length 188;  
Best Local Similarity 39.1%; Pred. No. 3.4e-16;  
Matches 43; Conservative 7; Mismatches 30; Indels 30; Gaps 2;  
  
Qy 68 WGPPEPLPYSRAFEGEGASARPR-----CCRNGSTCVLGSFCVCPAH 108  
Db 52 WPOEEP-----AIRPRSSQVRPPMGIQHSKELNRTCCCLNGTCLMGSCFACPPS 100  
  
Qy 109 FTGRYCEHDORRSECCGALHGHAWTLRACHLCRCIFGALHCLPLQTPDRCD 158  
Db 101 FYGRNCEHDVRKENCSCVPHDWTLPKKCSLCKCMHGLRCFPOAFLPGCD 150  
  
RESULT 14  
US-08-154-198-3  
; Sequence 3, Application US/08154198  
; Patent No. 5620866  
; GENERAL INFORMATION:  
; APPLICANT: SALOMON, David S.  
; APPLICANT: PERSICO, Maria G.  
; TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
;; COMPUTER READABLE FORM: disk  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/154,198  
;; FILING DATE: 17-NOV-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/749,001  
;; FILING DATE: 23-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bastian, Kevin L.  
;; REGISTRATION NUMBER: 34,774

; REFERENCE/DOCKET NUMBER: 15280-63-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 188 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-154-198-3

Query Match

Best Local Similarity 39.1%; Score 233; DB 1; Length 188;

Matches 43; Conservative 7; Mismatches 30; Indels 30; Gaps 2;

QY 68 WGPEEPLPYSRAFEGEGASARPR-----CCRNGGTCVLGSGFCVCPAH 108

DB 52 WPOEEP-----AIRPRSSQVRPPMGIOHSHKELNRTCCCLNGGTCMLGSGFCACPPS 100

QY 109 FTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158

DB 101 FYGRNCEHDVVRKENCQSVPHDTWLPKKCSLCKCMWHGQLRCFFQOAFPLPGCD 150

RESULT 15

US-08-463-335-3

; Sequence 3, Application US/08463335

; Patent No. 5650285

; GENERAL INFORMATION:

; APPLICANT: Salomon, David S.

; APPLICANT: Persico, Maria G.

; TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DABBY & CUSHMAN

; STREET: 1615 L Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/463,335

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/749,001

; FILING DATE: 23-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Scott, Watson T.

; REGISTRATION NUMBER: 26,581

; REFERENCE/DOCKET NUMBER: WTS/5683/91630/SRL

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3000

; TELEFAX: (202) 822-0944

; TELEX: 248453 CUSH

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 188 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-463-335-3

Query Match

Best Local Similarity 39.1%; Score 233; DB 1; Length 188;

Matches 43; Conservative 7; Mismatches 30; Indels 30; Gaps 2;

QY 68 WGPEEPLPYSRAFEGEGASARPR-----CCRNGGTCVLGSGFCVCPAH 108

DB 52 WPOEEP-----AIRPRSSQVRPPMGIOHSHKELNRTCCCLNGGTCMLGSGFCACPPS 100

QY 109 FTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158

DB 101 FYGRNCEHDVVRKENCQSVPHDTWLPKKCSLCKCMWHGQLRCFFQOAFPLPGCD 150

Search completed: September 7, 2006, 12:00:45

Job time : 50 secs